

83384

From: Chan, Christina  
 Sent: Tuesday, December 31, 2002 1:08 PM  
 To: Holleran, Anne; STIC-Biotech/ChemLib  
 Subject: RE: RUSH sequence search for 09/806,301

**Please rush. Thanks**

Chris Chan  
 TC 1600 New Hire Training Coordinator and SPE 1644  
 308-3973  
 CM-1, 9B19

Point of Contact:  
 Mona Smith  
 Technical Information Specialist  
 CM1 6A01  
 Tel: 308-3278

-----Original Message-----

From: Holleran, Anne  
 Sent: Tuesday, December 31, 2002 1:06 PM  
 To: Chan, Christina  
 Subject: RUSH sequence search for 09/806,301

Please approve and forward to STIC this RUSH sequence search request. This is an amendment due this biweek. Thanks.

Please search the following:

commercial and interference databases search of SEQ ID NO: 2(aa)

commercial and interference databases **oligomer** search of SEQ ID NO: 2(aa)

Anne Holleran  
 AU: 1642  
 Tel: 308-8892  
 RM: 8e03

mailbox: 8e12

TYPE OF SEARCH:

Searcher: M. Smith  
 Phone: \_\_\_\_\_  
 Location: \_\_\_\_\_  
 Date Picked Up: 1/2/03  
 Date Completed: 1/3/03  
 Searcher Prep/Review: 2  
 Clerical: \_\_\_\_\_  
 Online time: 7

NA Sequences: \_\_\_\_\_  
 AA Sequences: 2  
 Structures: \_\_\_\_\_  
 Bibliographic: \_\_\_\_\_  
 Litigation: \_\_\_\_\_  
 Full text: \_\_\_\_\_  
 Patent Family: \_\_\_\_\_  
 Other: \_\_\_\_\_

VENDOR/COST (where applic.)

STN: \_\_\_\_\_  
 DIALOG: \_\_\_\_\_  
 Questel/Orbit: \_\_\_\_\_  
 DRLink: \_\_\_\_\_  
 Lexis/Nexis: \_\_\_\_\_  
 Sequence Sys.: \_\_\_\_\_  
 WWW/Internet: \_\_\_\_\_  
 Other (specify): \_\_\_\_\_

Point of Contact  
Mons Smith  
Technical Information Specialist  
OMI 6A01  
Tel: 308-3258

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:53:07 : Search time 29 Seconds

(without alignments)  
639,457 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450  
Sequence: 1 MKLSVCLLVLTALCCYQAN.....LQKRSIAEVLVILKKCSV 90

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_21: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp Vertebrate: \*  
14: sp Unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result, being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249	55.3	90	6	09GK67
2	245	54.4	96	6	08WMS2
3	231.5	50.2	91	6	09GK66
4	226	50.2	90	6	09GK65
5	91	20.2	95	4	08TD33
6	85	18.9	96	11	08VD96
7	78.5	17.4	317	11	08VH6
8	77.5	17.2	94	11	005702
9	70.5	15.7	320	11	08VF26
10	69	15.3	167	11	09QWLS
11	69	15.3	1622	10	048908
12	69	15.3	1623	10	048907
13	69	15.3	1623	10	064590
14	68.5	15.2	1623	10	022449
15	68	15.1	290	10	08W3C2
16	67	14.9	74	10	08W2V1

17	66.5	14.8	434	5	09VZA6	09VZA6 drosophila
18	66.5	14.8	578	5	09XG30	09XG30 caenorhabdt
19	66	14.7	102	16	08U5C3	08U5C3 agrobacteri
20	65.5	14.6	310	5	097466	097466 trypanosoma
21	65.5	14.6	310	5	096649	096649 trypanosoma
22	65.5	14.6	415	4	09Y614	09Y614 homo sapien
23	65.5	14.6	415	6	095JX8	095JX8 macaca fasc
24	65	14.4	470	10	08S9A4	08S9A4 phaseolus a
25	64	14.2	213	5	09VBO4	09VBO4 drosophila
26	64	14.2	366	5	09U0W2	09U0W2 leishmania
27	64	14.2	797	10	09FW44	09FW44 arabidopsis
28	63	14.0	115	11	09DAK3	09DAK3 mus musculu
29	63	14.0	446	4	096EF4	096EF4 homo sapien
30	63	14.0	446	4	09NVH3	09NVH3 homo sapien
31	63	14.0	473	4	09H384	09H384 homo sapien
32	63	14.0	676	4	09BQ70	09BQ70 homo sapien
33	63	14.0	735	4	09H7V5	09H7V5 homo sapien
34	63	14.0	756	4	096ST4	096ST4 homo sapien
35	63	14.0	796	4	09P217	09P217 homo sapien
36	63	14.0	1354	10	0948F4	0948F4 oryza sativ
37	63	14.0	1862	10	094104	094104 oryza sativ
38	63	14.0	2029	5	09VD07	09VD07 drosophila
39	62.5	13.9	90	13	09PWA6	09PWA6 gallus gall
40	62.5	13.9	90	13	0910C9	0910C9 gallus gall
41	62.5	13.9	371	5	016474	016474 caenorhabdt
42	62.5	13.9	844	3	096X45	096X45 neurospora
43	62.5	13.9	929	16	098R55	098R55 mycoplasma
44	62	13.8	155	5	09V6U0	09V6U0 drosophila
45	62	13.8	167	4	09UED4	09UED4 homo sapien

## ALIGNMENTS

### RESULT 1

ID	09GK67	PRELIMINARY:	PRT:	90 AA.
AC	09GK67:			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Lipophilin AL.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	TISSUE=LACRIMAL GLAND;			
RA	Zhao C., Nguyen T.X., Lehrer R.I.;			
RT	"Rabbit Lipophilins."			
RL	Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF308614; AAC42802.1; -			
DR	InterPro: IPR000329; Uterogloblin.			
DR	Pfam: PF01099; Uterogloblin; 1.			
DR	SMART: SM00096; UMG; 1.			
SO	SEQUENCE 90 AA; 9762 MW; 6034F9540C1FF742 CRC64;			

Query Match 55.3%; Score 749; DB 6; Length 90;  
Best local Similarity 56.7%; Pred. I/O. 3.5e-22;  
Matches 51; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY	1	MKLSVCLLVLTALCCYQANAERCPALVSELDFFFLSEFLFKLSLAKFPAPPEAVAAKL 60
DB	1	MKLSVCLLVLTALCCYQANAERCPALVSELDFFFLSEFLFKLSLAKFPAPPEAVAAKL 60
QY	61	GVRKCTDOMSLQKRSIAEVLVILKKCSV 90
DB	61	QVKECDDEIDKGRVLIANVLTKIVKCAI. 90
RESULT 2		
Q8WMS2		

ID 08WMS2 PRELIMINARY; PRT; 96 AA.  
 AC 08WMS2:  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Lipophilin AL2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LACRIMAL GLAND;  
 RA Lind-Ayres M.R., Crow J.M., Steelman C.A., Nelson J.D.,  
 RA Remington S.G.;  
 RT "Lipophilin AL2 of the male rabbit lacrimal gland";  
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY063770; AAI40859.1;  
 DR InterPro: IPR000329; Uteroglobulin.  
 DR Pfam: PF01099; Uterogloblin; 1.  
 SQ SEQUENCE 96 AA: 10510 MW: 48EC2972DDEA78C4 CRC64;

Query Match 54.4%; Score 245; DB 6; Length 96;  
 Best Local Similarity 52.8%; Pred. No. 11e-21;  
 Matches 47; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSLAKFDAPPEAVAAKL 60  
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSLAKFDAPPEAVAAKL 60  
 OY 61 GVKRCTDMSLOKRSLLAEVLVKILKCS 89  
 DB 61 NVKRCVNEISLGLKRLIERILGEVLTECS 89

## RESULT 3

ID 09GK66 PRELIMINARY; PRT; 91 AA.  
 AC 09GK66:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Lipophilin AS.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SUBMAXILLARY;  
 RA Zhao C., Nguyen T.X., Lehrer R.I.;  
 RT "Rabbit Lipophilins";  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF308615; AAG42803.1;  
 DR InterPro: IPR000329; Uterogloblin.  
 DR Pfam: PF01099; Uterogloblin; 1.  
 DR PRINTS: PR00486; UTEROGLOBIN.  
 DR SMART: SMO0096; UTG; 1.  
 SQ SEQUENCE 91 AA: 9723 MW: 5790CD0B813554C4 CRC64;

Query Match 51.4%; Score 231.5; DB 6; Length 91;  
 Best Local Similarity 51.6%; Pred. No. 4.4e-20;  
 Matches 47; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSLAKFDAPPEAVAAKL 60  
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSLAKFDAPPEAVAAKL 60  
 OY 61 GVKRCTDMSLOKRSLLAEVLVKI-LKKCSV 90  
 DB 61 GVKRCTDKMSLGRVLFGEIVLRTCTL 91

RESULT 4  
 ID 09GK65 PRELIMINARY; PRT; 90 AA.  
 AC 09GK65:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Lipophilin BL.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LACRIMAL GLAND;  
 RA Zhao C., Nguyen T.X., Lehrer R.I.;  
 RT "Rabbit Lipophilins";  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF308616; AAG42804.1;  
 DR InterPro: IPR000329; Uterogloblin.  
 DR Pfam: PF01099; Uterogloblin; 1.  
 DR PRINTS: PR00486; UTEROGLOBIN.  
 SQ SEQUENCE 90 AA: 9943 MW: 410900DF7F3EB1BC CRC64;

Query Match 50.2%; Score 226; DB 6; Length 90;  
 Best Local Similarity 51.1%; Pred. No. 2e-19;  
 Matches 46; Conservative 17; Mismatches 27; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSLAKFDAPPEAVAAKL 60  
 DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSLAKFDAPPEAVAAKL 60  
 OY 61 GVKRCTDMSLOKRSLLAEVLVKILKCSV 90  
 DB 61 TVKCTDGMPEFRKRNILAGALGEVYLCV 90

## RESULT 5

ID 08TD33 PRELIMINARY; PRT; 95 AA.  
 AC 08TD33:  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Putative ligand binding protein RYD5.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bingle C.D.;  
 RT "Human RYD5, a new secretogloblin";  
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY026938; AAK08972.1;  
 SQ SEQUENCE 95 AA: 10457 MW: F629AF06C96D2392 CRC64;

Query Match 20.2%; Score 91; DB 4; Length 95;  
 Best Local Similarity 29.5%; Pred. No. 0.0027;  
 Matches 28; Conservative 16; Mismatches 35; Indels 16; Gaps 2;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFIS-----EPLKLSLAKFD 50  
 DB 1 MKGSRALLLVLTALCCYQNAEFCPALVSELDFFIS-----ICRWATGEDNDEFMDLQTLVOTPELYEGTLGKYN 54  
 OY 51 APPEAVAAKLGVKRCIDMSLOKRSLLAEVLVKIL 85  
 DB 55 VNEDAKAAATELKSQRDLQPMKAEVLKLVOL 89

RESULT 6  
 ID 08VD96 PRELIMINARY; PRT; 96 AA.  
 AC 08VD96:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Lipophilin BL.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LACRIMAL GLAND;  
 RA Zhao C., Nguyen T.X., Lehrer R.I.;  
 RT "Rabbit Lipophilins";  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF308616; AAG42804.1;  
 DR InterPro: IPR000329; Uterogloblin.  
 DR Pfam: PF01099; Uterogloblin; 1.  
 DR PRINTS: PR00486; UTEROGLOBIN.  
 SQ SEQUENCE 90 AA: 9943 MW: 410900DF7F3EB1BC CRC64;

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AC 08VD96;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE CC10 protein precursor.
GN CC10.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
NCBI_TaxID=10036;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Gutterer-Sagal R., Nieto A.;
RT "Cloning and sequencing of a cDNA encoding hamster uteroglobin/clara
cell 10 kDa protein."
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; L37041; AAL31349.1;
DR InterPro; IPR003628; Uteroglobin_sub.
DR InterPro; IPR000329; Uteroglobin.
DR Pfam; PF01099; Uteroglobin; 1.
DR ProDom; PD012475; Uteroglobin_sub; 1.
DR SMART; SM00096; UTE; 1.
DR PROSITE; PS00404; UTEROGLBIN_2; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 96 AA; 10509 MW; 5EB9CBB046143389 CRC64;

Query Match 18.9%; Score 85; DB 11; Length 96;
Best Local Similarity 24.4%; Pred. No. 0.014;
Matches 21; Conservative 27; Mismatches 36; Indels 2; Gaps 2;

QY 1 MKLSVCLLVTLALCCQANAEPCPALVSELDFFFT-SEPLFKLSLAKDPAPPAVAK 59
DB 1 MKLAITAAVVAWLVCCSSASSDTCPPFP-QVLEFLFMSSESYPAALKFYNPGSDLDQSG 59
QY 60 LGVRCRTDQMSLQKRSLSIAEVLVKIL 85
DB 60 TOLKKLVDTLPQKTRNMIMKLSFTIL 85

RESULT 7
Q8VFH6 PRELIMINARY; PRT; 317 AA.
ID 08VFH6;
AC 08VFH6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Olfactory receptor MOR14-8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RT Nat. Neurosci. 0:0-0(2002).
GN [2]
OS SEQUENCE FROM N.A.
RP Adams M.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073550; AAL61213.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_P1_2; 1.
KW Receptor.
SQ SEQUENCE 317 AA; 35896 MW; 6C550A33DD277D24 CRC64;

Query Match 17.4%; Score 78.5; DB 11; Length 317;

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Best Local Similarity 25.3%; Pred. No. 0.28;
Matches 25; Conservative 13; Mismatches 22; Indels 39; Gaps 5;

QY 1 MKLSVCLLVTLALCCQYQ-----NAECPALVSELDFFFT-SEPLFKSL 46
DB 133 MSSKVC---QTLVLCWSAGLLIPLPLFLNRFCD---SNVIDYFCDASPLIKIS- 185
QY 47 AKDPAPPAVAARKGVRCRTDQMSLQKRSLSIAEVLVKIL 95
DB 186 -----GSDTWLEQLVAVCAVLPFIL 306

RESULT 8
Q05702 PRELIMINARY; PRT; 94 AA.
ID 005702;
AC 005702;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
DE Potential ligand-binding protein.
GN RVD5.
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10117;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISCHER; TISSUE=OLFACTORY EPITHELIUM;
RX MEDLINE=92007724; Pubmed=1915264;
RA Dear T.N., Boehm T., Reverte E.B., Rabbits T.H.;
RT "Novel genes for potential ligand-binding proteins in subregions of
the olfactory mucosa."
RT EMBL; J10-2813-2819(1991).
DR InterPro; IPR000329; Uteroglobin.
DR SMART; SM00096; UTE; 1.
SQ SEQUENCE 94 AA; 10401 MW; 25A4BBB4977E247 CRC64;

Query Match 17.2%; Score 77.5; DB 11; Length 94;
Best Local Similarity 28.4%; Pred. No. 0.11;
Matches 25; Conservative 15; Mismatches 45; Indels 3; Gaps 2;

QY 1 MKLSVCLLVTLALC-CYQANAEPCPALVSELDFFFTSEPLFKLSLAKDPAPPAVA 57
DB 1 MKSSALIVALTVCICGLPRAEDNPFMEFLDTLVGVPEELXPPLKYNVNDAKA 60
QY 58 AKLGKRCRTDQMSLQKRSLSIAEVLVKIL 85
DB 61 ALTELKSCIDELQPVHKEQLVILVOYL 88

RESULT 9
Q8VF26 PRELIMINARY; PRT; 320 AA.
ID 08VF26;
AC 08VF26;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE Olfactory receptor MOR14-11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
OX
RN [1]
RP SEQUENCE FROM N.A.
RC Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RT Nat. Neurosci. 0:0-0(2002).
GN [2]
OS SEQUENCE FROM N.A.
RP Adams M.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY073715; AAL61378.1;

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OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lu Y.-P., Li Z.-S., Drodowicz Y.M., Hortensteiner S., Martinoia E.,  
 RA Rea P.A.;  
 RT "AtMRP2, an Arabidopsis ATP-binding cassette transporter able to  
 RT transport glutathione S-conjugates and chlorophyll catabolites:  
 RT functional comparisons with AtMRP1.";  
 RL Plant Cell 10:1-18(1998).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.  
 DR EMBL: AF020288; AAC04245.1; -.  
 DR HSSP: P13569; INBD.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR001140; ABCtransprtrTM.  
 DR InterPro: IPR003439; ABC.transprtr.  
 DR Pfam: PF00664; ABC\_membrane; 2.  
 DR Pfam: PF00005; ABC\_tran; 2.  
 DR ProDom: PD000006; ABC\_transprtr; 2.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER; 2.  
 DR ATP-binding; Hydrolase; Transporter.  
 KW SEQUENCE 1623 AA; 182073 MW; 963087B048999970 CRC64;  
 SO

Query Match 15.3%; Score 69; DB 10; Length 1623;  
 Best Local Similarity 36.5%; Pred. No. 19;  
 Matches 27; Conservative 9; Mismatches 22; Indels 16; Gaps 5;

QY 3 LSVCLLVLTALCCYQANAEFCALVSELDFFF-----ISEPLFKL----SLAKFDA 51  
 ID 022449 PRELIMINARY: PRT; 1623 AA.  
 AC 022449;  
 DT 01-JAN-1998 (TRENBLREL. 05, Created)  
 DT 01-JAN-1998 (TRENBLREL. 05, last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)  
 DE Multidrug resistance-associated protein 2.  
 GN ATMRP2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhahn T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Motilal K.S.,  
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Niernman W.C., White O., Eisen J.A.,  
 RA Salberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 402:761-768(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Lin X.;  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.  
 DR EMBL: AC003096; AAC16268.1; -.  
 DR HSSP: P13569; INBD.

RESULT 13  
 064590

ID 064590 PRELIMINARY: PRT; 1623 AA.

AC 064590;  
 DT 01-AUG-1998 (TRENBLREL. 07, Created)  
 DT 01-AUG-1998 (TRENBLREL. 07, last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)  
 DE ABC transporter (AtMRP2).  
 GN ATG34660.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldhahn T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Konning C.M., Koo H., Motilal K.S.,  
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Niernman W.C., White O., Eisen J.A.,  
 RA Salberg S.L., Fraser C.M., Venter J.C.;  
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 402:761-768(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Lin X.;  
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.  
 DR EMBL: AC003096; AAC16268.1; -.  
 DR HSSP: P13569; INBD.

DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR001140; ABCtransprtrTM.  
 DR InterPro: IPR003439; ABC.transprtr.  
 DR Pfam: PF00664; ABC\_membrane; 2.  
 DR Pfam: PF00005; ABC\_tran; 2.  
 DR ProDom: PD000006; ABC\_transprtr; 2.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER; 2.  
 DR ATP-binding; Transporter.  
 KW SEQUENCE 1623 AA; 182129 MW; F074F06ED7A1D47 CRC64;  
 SO

Query Match 15.3%; Score 69; DB 10; Length 1623;  
 Best Local Similarity 36.5%; Pred. No. 19;  
 Matches 27; Conservative 9; Mismatches 22; Indels 16; Gaps 5;

QY 3 LSVCLLVLTALCCYQANAEFCALVSELDFFF-----ISEPLFKL----SLAKFDA 51  
 ID 022449 PRELIMINARY: PRT; 1623 AA.  
 AC 022449;  
 DT 01-JAN-1998 (TRENBLREL. 05, Created)  
 DT 01-JAN-1998 (TRENBLREL. 05, last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, last annotation update)  
 DE Multidrug resistance-associated protein 2.  
 GN ATMRP2.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-LANDSBERG ERECTA;  
 RA MEDLINE=98189246; PubMed=9528668;  
 RA Martin E., Leonhardt N., Vavasseur A., Forestier C.;  
 RT "Cloning of AtMRP1, an Arabidopsis thaliana cDNA encoding a homologue  
 RT of the mammalian multidrug resistance-associated protein.";  
 RL Biochim. Biophys. Acta 1369:7-13(1998).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.  
 DR EMBL: AF014960; AAC49988.1; -.  
 DR HSSP: P13569; INBD.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR001140; ABCtransprtrTM.  
 DR InterPro: IPR003439; ABC.transprtr.  
 DR Pfam: PF00664; ABC\_membrane; 2.  
 DR Pfam: PF00005; ABC\_tran; 2.  
 DR ProDom: PD000006; ABC\_transprtr; 1.  
 DR SMART: SM00382; AAA; 1.  
 DR PROSITE: PS00211; ABC\_TRANSPORTER; 2.  
 DR ATP-binding; Transporter.  
 KW SEQUENCE 1623 AA; 181968 MW; 1D17ACE1D0578D33 CRC64;  
 SO

Query Match 15.2%; Score 68.5; DB 10; Length 1623;  
 Best Local Similarity 35.5%; Pred. No. 22;  
 Matches 27; Conservative 6; Mismatches 20; Indels 23; Gaps 5;

QY 9 LVTLALCCYQ-----ANAEFCALVSELDFFF-----ISEPLFKL----SLAKF 49  
 ID 44 LVLVLCVLRIMVLTLDKDKVERFC--LRSLRYNYFLALAAVATAPLRLINGISVLD 101  
 DB 44 LVLVLCVLRIMVLTLDKDKVERFC--LRSLRYNYFLALAAVATAPLRLINGISVLD 101  
 QY 50 DAP--PEVAARKIGVK 63  
 ID 102 DGGPLPPEAFGLGK 117  
 DB 102 DGGPLPPEAFGLGK 117

```

RESULT 15
ID      08W3C2      PRELIMINARY:      PRT:      290 AA.
AC      08W3C2.
DT      01-MAR-2002 (TRENBLREL. 20. Created)
DT      01-MAR-2002 (TRENBLREL. 20. Last sequence update)
DT      01-JUN-2002 (TRENBLREL. 21. Last annotation update)
DE      Putative polypeptide (Hypothetical 33.4 kDa protein).
GN      OSJNBA0046102.13 OR OJ136E01.1.
OS      Oryza sativa (Rice)
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=4530;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA      Saski C., Henry D., Oates R., Simmons J.;
RT      "Rice Genomic Sequence.";
RL      Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=NIPPONBARE;
RA      McCombie W.R., de la Bastide M., Splegel L., Preston R., Kirchoff K.,
RA      Kuhl K., Nascimento L., Zuberer T., Balija V., Bell M., Baker J.,
RA      Santos L., Miller B., Katzenberger F., Muller S., King L., Yang C.,
RA      O'Shaughnessy A., Palmer L., Dedhia N.;
RT      "Genomic sequence for Oryza sativa, Nipponbare strain, clone
RT      OJ136E01, from chromosome 10, complete sequence.";
RL      Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC079632; AAL73569.1; -
DR      EMBL; AC108883; AAM08628.1; -
DR      InterPro; IPR005162; Retrotrans_gag.
DR      Pfam; PF03732; Retrotrans_gag; 1.
KW      Hypothetical protein; Polypeptide.
SQ      SEQUENCE 290 AA; 33370 MW; 93A623E60C8C5909 CRC64;

Query Match      15.1%; Score 68; DB 10; Length 290;
Best Local Similarity 36.4%; Pred. No. 4.6;
Matches 20; Conservative 8; Mismatches 23; Indels 4; Gaps 2;

QY      18 QANAEF--CPALVSELDFFFTISEPLFKLSLAKFDAPP--EAVAAKLGVKRCTDQ 68
DB      66 QQNDQFGPPSHVSKLDFLRIOPTFSSTNPMENDWMLRAIEKKTLLQCNDQ 120

```

Search completed: January 2, 2003, 14:55:18  
 Job time : 32 secs





XX Gentz RL, Ni J, Yu G;  
 XX  
 XX WPI: 1997-480206/44.  
 DR N-PSDB: AAT94831.  
 XX  
 PT Human endometrial specific steroid-binding factor I, II and III -  
 PT used to treat inflammation, asthma, rhinitis, cystic fibrosis,  
 PT allergy disease, neoplasia, atopy etc.  
 PS  
 PS Claim 18; Page 63-64; 92pp; English.  
 CC This sequence comprises human endometrial specific steroid binding  
 CC factor II (ESF II), a protein that inhibits phospholipase A2  
 CC activity, binds to polychlorinated biphenyl compounds, reduces  
 CC foreign protein antigenicity, inhibits monocyte and neutrophil  
 CC chemotaxis and phagocytosis, inhibits platelet aggregation,  
 CC regulates eicosanoid levels in the human uterus and controls the  
 CC growth of endometrial cells. The amino acid sequence was deduced  
 CC from a cDNA clone (see AAT94831) derived from cycloheximide-treated  
 CC CEM cells. ESF I (see AAW35802) and ESF III (see AAW35804) are also  
 CC claimed. Human ESF II has about 49% identity with rat prostatic  
 CC steroid-binding protein. Recombinant ESF I, II and III can be  
 CC expressed in host cells for use in claimed methods (a) for treating  
 CC a patient in need of ESF I, II or III (including expression of the  
 CC polypeptide in vivo) and (b) for identifying compounds which bind  
 CC to and inhibit activation of the ESF polypeptide. hESF I, II and  
 CC II may be used to treat inflammation, asthma, rhinitis, cystic  
 CC fibrosis, allergy disease, neoplasia and atopy.  
 CC  
 SQ Sequence 90 AA:  
 Query Match 100.0%; Score 90; DB 19; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAKL 60  
 Db 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAKL 60  
 QY 61 GVKRCTDQMSLQKRSLSLAELVLTILKKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLSLAELVLTILKKCSV 90  
 RESULT 2  
 AAW59776  
 ID AAW59776 standard; Protein: 90 AA.  
 XX  
 AC AAW59776;  
 XX  
 DT 12-OCT-1998 (first entry)  
 XX  
 DE Amino acid sequence of the human steroid binding protein C1.  
 XX  
 KW Human steroid-binding protein C1; hSBP1; hSBP2; breast cancer; probe;  
 KW gene therapy vector; ribozyme; probe; hybridisation; amplification;  
 KW antibody; immunoassay.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9821331-A1.  
 XX  
 PD 22-MAY-1998.  
 XX  
 PF 07-NOV-1997; 97MO-US20674.  
 XX  
 PR 12-NOV-1996; 96US-0747547.  
 XX  
 PA (INCY-) INCYTE PHARM INC.  
 XX  
 PI Akerblom IE, Goli SK, Hawkins PR, Hillman JL, Murry LE;  
 XX

DR WPI: 1998-297935/26.  
 DR N-PSDB: AAV41579.  
 XX  
 PT New human steroid binding proteins C1 and C2 - useful for, e.g.  
 PT diagnosis, monitoring and treating breast cancer, and for drug  
 PT screening  
 PT  
 PS Claim 1; Fig 1; 70pp; English.  
 CC  
 CC This is the amino acid sequence of the human steroid-binding protein  
 CC C1 (hSBP1) used in the method of the invention for the diagnosis,  
 CC monitoring and treatment of breast cancer. hSBP1 and hSBP2 are useful  
 CC as markers for breast cancer, i.e. measuring levels of hSBP1 and hSBP2  
 CC used for diagnosis or monitoring the disease, to identify subjects  
 CC at risk and to discriminate between different forms of cancer for  
 CC selection of appropriate therapies. They may also be used for drug  
 CC screening. Nucleic acids encoding hSBP1 and hSBP2 can be used in gene  
 CC therapy vectors to overexpress the steroid-binding proteins, preventing  
 CC binding of steroids, or antisense sequences, ribozymes. Their nucleic  
 CC acids can also be used for the diagnosis and monitoring (by quantifying  
 CC expression of hSBP), as source of probes for hybridisation and  
 CC amplification of genomic or related sequences for studying regulation of  
 CC gene function and for mapping the genomic sequence. Antibodies are used  
 CC as diagnostic reagents in standard immunoassays for hSBP.  
 CC  
 SQ Sequence 90 AA:  
 Query Match 100.0%; Score 90; DB 19; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAKL 60  
 Db 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFAPPAVAKL 60  
 QY 61 GVKRCTDQMSLQKRSLSLAELVLTILKKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLSLAELVLTILKKCSV 90  
 RESULT 3  
 AAW54271  
 ID AAW54271 standard; Protein: 90 AA.  
 XX  
 AC AAW54271;  
 XX  
 DT 29-JUL-1998 (first entry)  
 XX  
 DE BU101 antigenic peptide epitope 1.  
 XX  
 KW BU101; breast cancer; diagnosis; prevention; treatment; gene therapy;  
 KW immunisation; drug screening; epitope.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9807857-A1.  
 XX  
 PD 26-FEB-1998.  
 XX  
 PF 19-AUG-1997; 97MO-US14665.  
 XX  
 PR 15-AUG-1997; 97US-0912276.  
 XX  
 PR 19-AUG-1996; 96US-0697105.  
 XX  
 PA (ABBO) ABBOTT LAB.  
 XX  
 PI Billing-medel PA, Cohen M, Colpits TL, Friedman PN;  
 PI Gordon J, Granadosen, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-rapp L, Russell JC, Stroupe SD;  
 XX  
 DR WPI: 1998-169161/15.  
 DR N-PSDB: AAV26461.  
 XX

PT New Bu101 protein over-expressed in breast cancer - useful for, e.g.  
 PT diagnosis, treatment and prevention of breast cancer

PS Claim 17; Page 90; 105pp; English.

XX This represents a Bu101 polypeptide sequence. Bu101 is a member of the  
 CC uteroglobin family of proteins and is over-expressed in breast cancer.  
 CC Cells transformed with a recombinant expression system comprising a  
 CC sequence derived from the Bu101 open reading frame and with at least 50  
 CC percent identity to the sequences shown in AAV26458 to AAV26461 are used  
 CC to produce Bu101 polypeptides containing at least 1 epitope. These are  
 CC used to detect Bu101-specific antibodies which are used correspondingly  
 CC to detect Bu101 antigens. The Bu101 polynucleotide sequences can be used  
 CC in a method for detecting the presence of a target Bu101 polynucleotide.  
 CC The various assays are used for diagnosis, prognosis, staging, monitoring,  
 CC monitoring, treating and preventing diseases of the breast (especially  
 CC cancer and its metastases), and also for determining susceptibility. The  
 CC Bu101 polypeptides are also useful in drug screening, e.g. to identify  
 CC antagonists of Bu101, potentially useful therapeutically and as targets  
 CC for therapy. The antibodies are also useful for targeted drug delivery  
 CC and therapeutically to neutralise Bu101 polypeptides. Fragments of the  
 CC Bu101 nucleic acid are useful as probes and primers, e.g. for detection  
 CC of altered gene expression or in fluorescent in situ hybridisation, also  
 CC in gene therapy to generate antisense or ribozyme molecules or for  
 CC genetic immunisation.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 19; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISBPFLKSLAKDPAPPAVAARKL 60  
 DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISBPFLKSLAKDPAPPAVAARKL 60  
 OY 61 GVKRCTDQMSLOKRSLSIAEVLVKILKCSV 90  
 DB 61 GVKRCTDQMSLOKRSLSIAEVLVKILKCSV 90

RESULT 4  
 AAM89613  
 ID AAM89613 standard; Protein; 90 AA.

XX AAM89613;

DT 25-MAR-1999 (first entry)

DE Endometrial steroid binding protein II.

KM Endometrial steroid binding protein II; ESBPII; cancer; detection;  
 KM endometriosis; endometrial fibroid; mammary cancer.

OS Homo sapiens.

PN WO9856248-A1.

PD 17-DEC-1998.

PF 09-JUN-1998; 98WO-US12053.

PR 09-JUN-1997; 97US-0049015.

PA (SMITK ) SMITHKLINE BEECHAM CORP.

PI Schmidt CJ, Wang X;

DR WPI: 1999-080843/07.  
 DR N-PSDB; AAX00069.

PT Treatment of endometrial cancer, mammary cancer, endometriosis or  
 PT endometrial fibroids - comprises administering endometrial steroid

PT binding protein II antagonist

PS Disclosure; Page 13; 19pp; English.

XX A method has been developed for the treatment of endometrial cancer,  
 CC mammary cancer, endometriosis or endometrial fibroids. The method  
 CC comprises administering endometrial steroid binding protein II (ESBPII)  
 CC antagonist. Also described in the present invention are: (1) a method  
 CC for diagnosing the above mentioned diseases comprising analysing the  
 CC abnormally high level of ESBPII polypeptide in cells, tissues and bodily  
 CC fluids; and (2) a diagnostic method for the diseases described above  
 CC comprising analysing the abnormally high or low transcription level of  
 CC ESBPII in cells, tissues and bodily fluids. The methods can be used to  
 CC diagnose, treat, and monitor the progression, remission or recurrence of  
 CC abnormal cell growth, such as cancers, especially endometrial and  
 CC mammary cancer, and endometriosis and endometrial fibroids. The present  
 CC sequence represents ESBPII, from the present invention.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 20; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISBPFLKSLAKDPAPPAVAARKL 60  
 DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISBPFLKSLAKDPAPPAVAARKL 60  
 OY 61 GVKRCTDQMSLOKRSLSIAEVLVKILKCSV 90  
 DB 61 GVKRCTDQMSLOKRSLSIAEVLVKILKCSV 90

RESULT 5  
 AAB13787  
 ID AAB13787 standard; Protein; 90 AA.

XX AAB13787;

DT 20-JUN-2001 (first entry)

DE Human Bu101.

KM Human; breast cancer; breast disease detection; mammaglobin;  
 KM uteroglobin; Bu101; endometrial; cytostatic.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 53

FT /label= Leu /note= "Encoded by CTG in polymorphic variant"

PN WO200035950-A2.

PD 22-JUN-2000.

PF 20-DEC-1999; 99WO-US30489.

PR 18-DEC-1998; 98US-0215818.

PA (ABBO ) ABBOTT LAB.

PI Colpitts TL, Russell JE;

DR WPI: 2000-442366/38.

PT Multimeric polypeptide antigen and antibody specific to the antigen are  
 PT useful for diagnosing, detecting and treating breast cancer -

PS Claim 1; Page 124; 124pp; English.

CC BU101 is a member of the uteroglobin protein family. The present  
 CC sequence is the protein sequence for human BU101. The present  
 CC invention relates to a multimeric polypeptide antigen, which comprises  
 CC of the present sequence and mamaglobin polypeptide (AAB13786).  
 CC Mamaglobin is another uteroglobin protein. The presence of multimeric  
 CC polypeptide antigen in a test sample can be used as the basis for a test  
 CC to diagnose breast disease e.g. breast cancer, in a patient. The  
 CC detection can be carried out using antibodies specific for the multimeric  
 CC polypeptide antigen. The present sequence can either have a Pro or Leu  
 CC residue at position 53, since the coding sequence has a single  
 CC nucleotide T/C polymorphism at nucleotide position 254.  
 CC  
 XX Sequence 90 AA:  
 S0  
 Query Match 100.0%; Score 90; DB 21; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60  
 DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60  
 QY 61 GVKRCTDQMSIQKRSLSIAEVLVKILKCSV 90  
 DB 61 GVKRCTDQMSIQKRSLSIAEVLVKILKCSV 90  
 Db  
 RESULT 6  
 AAB07501  
 ID AAB07501 standard; Protein: 90 AA.  
 AC AAB07501:  
 DT 20-OCT-2000 (first entry)  
 DE Amino acid sequence of a human BU101 polypeptide.  
 XX  
 KW Human; BU101; breast disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200041516-A2.  
 PD 20-JUL-2000.  
 PE 19-JAN-2000; 2000WO-US01309.  
 PF 19-JAN-1999; 99US-0233693.  
 PR 19-JAN-1999; 99US-0233693.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-rapp L;  
 PI Russell JC, Scheffel CP, Stroupe SD;  
 XX  
 DR WPI: 2000-475906/41.  
 DR N-PSDB: AAA58880.  
 XX  
 PT Detecting presence of target BU101 polynucleotide in sample useful for  
 PT detection of breast cancer, comprises contacting sample with  
 PT BU101-specific polynucleotide and determining binding -  
 PT  
 XX  
 PS Claim 23; Page 125; 127pp; English.  
 XX  
 CC The present sequence represents a BU101 polypeptide. The BU101 gene is  
 CC transcribed from breast tissue. The specification describes a method for  
 CC detecting the presence of a target BU101 polynucleotide in a test  
 CC sample. The method comprises contacting the sample with at least one  
 CC BU101-specific polynucleotide (AAA58875-80), and detecting bound  
 CC polynucleotides. The method and BU101 polynucleotides are useful for  
 CC detecting the presence of BU101 polynucleotides. The methods may be  
 CC used for the diagnosis of breast disease, indicated by the formation  
 CC of complexes.

XX  
 S0 Sequence 90 AA:  
 Query Match 100.0%; Score 90; DB 21; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2,2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60  
 DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAKL 60  
 QY 61 GVKRCTDQMSIQKRSLSIAEVLVKILKCSV 90  
 DB 61 GVKRCTDQMSIQKRSLSIAEVLVKILKCSV 90  
 Db  
 RESULT 7  
 AAB03768  
 ID AAB03768 standard; Protein: 90 AA.  
 AC AAB03768:  
 DT 06-OCT-2000 (first entry)  
 DE Human endometrial specific steroid-binding factor II protein sequence.  
 XX  
 KW Endometrial specific steroid-binding factor; human; hESF; inflammation;  
 KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;  
 KW ecicosanoid level regulator; chemotaxis inhibitor; endometrial cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6066724-A.  
 PD 23-MAY-2000.  
 PE 21-MAR-1997; 97US-0821451.  
 PF 21-MAR-1996; 96US-0014724.  
 PR 21-MAR-1996; 96US-0014724.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Yu G, Gentz R, NI J;  
 PI  
 DR WPI: 2000-375600/32.  
 DR N-PSDB: AAA59729.  
 XX  
 PT Novel gene encoding human endometrial specific steroid-binding factor  
 PT I, II and III which is useful for treating asthma, rhinitis, cystic  
 PT fibrosis, airway disease and neoplasia -  
 PT  
 XX  
 PS Claim 1; Fig 2; 36pp; English.  
 XX  
 CC This invention relates to nucleic acid molecules encoding portions of the  
 CC human endometrial specific steroid-binding factors I, II, and III. Also  
 CC included in the invention are hESF I, II, and III polypeptide sequences.  
 CC The nucleotide sequence exhibit antiasmatic, antiinflammatory,  
 CC antiallergic, and cytostatic properties. The polynucleotides are used in  
 CC gene therapy to express hESF I, II and III polypeptides in vivo to treat  
 CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way  
 CC disease, neoplasia and atopy. The polynucleotides are also used to  
 CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce  
 CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis  
 CC and phagocytosis, inhibit platelet aggregation, regulate ecicosanoid  
 CC levels in the human uterus and control the growth of endometrial cells.  
 CC The polynucleotides are also useful for detecting complementary  
 CC polynucleotides as a diagnostic reagent. The hESF I, II and III  
 CC polynucleotides are used to detect complementary polynucleotides such as  
 CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III  
 CC associated with a dysfunction will provide a diagnostic tool that can  
 CC define diagnosis of a disease or susceptibility to a disease which  
 CC results from under-expression, over-expression or altered expression of  
 CC hESF I, II and III e.g. a susceptibility to inherited asthma and

CC endometrial cancer. They are also useful for chromosome identification.  
 CC The present sequence represents a hsf II protein sequence identified in  
 CC the invention.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 21; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVCLLVTLALCCYQANAEECPALVSELDFFIISBFLFKLSAKEDAPPEAVAAKL 60  
 DB 1 MKISVCLLVTLALCCYQANAEECPALVSELDFFIISBFLFKLSAKEDAPPEAVAAKL 60

QY 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90  
 DB 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90

RESULT 8  
 AAY84875

ID AAY84875 standard; Protein; 90 AA.

XX AAY84875;

DT 08-AUG-2000 (first entry)

DE A human endometrial specific steroid-binding protein II.

XX Human; endometrial specific steroid-binding protein II; ESBPII;  
 KW breast tumour; prostate cancer; gynaecological cancer; cancer;  
 KM endometrial cancer; ovarian cancer; uterine cancer.

XX Homo sapiens.

PN WO200020043-A1.

PD 13-APR-2000.

PF 05-OCT-1999; 99WO-US23252.

PR 05-OCT-1998; 98US-0103093.

PA (DIAD-) DIADENXUS LLC.

PI Macina RA;

DR WPI: 2000-303648/26.

DR N-PSDB: AAA14953.

PT Diagnosing, staging, monitoring, imaging and treating prostate and  
 PT gynaecological cancers by measuring levels of endometrial specific  
 PT steroid-binding protein (ESBP)II expression

PS Claim 6; Page 31-32; 35pp; English.

CC The present sequence represents a human endometrial specific steroid-  
 CC binding protein (ESBP) II. The ESBPII protein is overexpressed in  
 CC breast tumours. The specification describes a method for diagnosing  
 CC prostate or a gynaecological cancer. The method comprises measuring  
 CC levels of ESBPII in cells, tissues or body fluids of a patient, and  
 CC comparing this to levels from a normal control, where a variance in  
 CC levels indicates cancer. The method is used to diagnose, stage, monitor,  
 CC image or treat prostate or gynaecological cancer. The gynaecological  
 CC cancers include breast, endometrial, ovarian and uterine cancer.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 21; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVCLLVTLALCCYQANAEECPALVSELDFFIISBFLFKLSAKEDAPPEAVAAKL 60

DB 1 MKISVCLLVTLALCCYQANAEECPALVSELDFFIISBFLFKLSAKEDAPPEAVAAKL 60

QY 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90

DB 61 GVARCTDOMSLQKRSLSIAEVLVKILKCSV 90

RESULT 9

ID AAG65989 standard; Protein; 90 AA.

XX AAG65989;

DT 11-FEB-2002 (first entry)

DE Lipophilin B polypeptide.

KW Genetic subtraction; DNA microarray analysis; polymerase chain reaction;  
 KM cancer; B726P; Lipophilin B; mammaglobin.

XX Homo sapiens.

PN WO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR 20-JUL-2000; 2000US-219862P.

PR 27-JUL-2000; 2000US-221300P.

PR 18-DEC-2000; 2000US-256582P.

PA (CORI-) CORIXA CORP.

PI Houghton RL, Dillon DC, Molesh DA, Xu J, Zehentner B, Persing DH;

DR WPI: 2001-626449/72.

DR N-PSDB: AAI67269.

PT Identifying tissue (tumour)-specific polynucleotides overexpressed in  
 PT tissue of interest as compared to control tissue, for detecting cancer  
 PT cells in patient, comprises DNA microarray analysis or quantitative  
 PT polymerase chain reaction

PS Examples; Page 127; 127pp; English.

CC The invention relates to identifying tissue-specific polynucleotides (P)  
 CC that involves performing a genetic subtraction to identify pool of (P)  
 CC from tissue of interest (TI), performing DNA microarray analysis to  
 CC identify first subset of polynucleotides (SPI) at least 2-fold over  
 CC expressed in TI, and performing quantitative polymerase chain reaction  
 CC (PCR) analysis on SPI to identify second subset of (P). The method is  
 CC useful for determining the presence or absence of a cancer cell in a  
 CC patient, monitoring the progression of cancer in a patient using a  
 CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,  
 CC urine or a tumour biopsy sample. The methods are useful for determining  
 CC the presence or absence of or monitoring progression of prostate, breast,  
 CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,  
 CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present  
 CC sequence represents the lipophilin B polypeptide.

XX Sequence 90 AA;

Query Match 100.0%; Score 90; DB 22; Length 90;  
 Best Local Similarity 100.0%; Pred. No 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVCLLVTLALCCYQANAEECPALVSELDFFIISBFLFKLSAKEDAPPEAVAAKL 60  
 DB 1 MKISVCLLVTLALCCYQANAEECPALVSELDFFIISBFLFKLSAKEDAPPEAVAAKL 60

Qy 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90  
 ||||||||||||||||||  
 Db 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90

## RESULT 10

AAE07518  
 ID AAE07518 standard; Protein: 90 AA.

XX  
 AC AAE07518;

DT 06-NOV-2001 (first entry)

DE Human lipophilin B protein.

XX  
 KW Human lipophilin B; cytosolic; vaccine; gene therapy; uteroglobin;

KW cancer; breast; ovary; prostate.

XX  
 OS Homo sapiens.

XX  
 PN WO200158947-A1.

XX  
 PD 16-AUG-2001.

XX  
 PF 08-FEB-2001; 2001WO-US04439.

XX  
 PR 11-FEB-2000; 2000US-0183495.

XX  
 PR 28-JUN-2000; 2000US-0215735.

XX  
 PA (CORI-) CORIXA CORP.

XX  
 PI Carter D, Vedvick TS, Vailleve-Dougllass J, Houghton RL, Dillon DC;

XX  
 DR WPI: 2001-497069/54.

XX  
 DR N-PSDB: AAD13756.

XX  
 PT Novel isolated complex two lipophilin-like polypeptides linked by at

PT least one disulphide bond, used to treat or prevent breast, ovarian or

XX  
 PS prostate cancer -

XX  
 PS Example 5; Page 72; 91pp; English.

XX  
 CC The invention relates to a complex comprising a lipophilin-like  
 CC polypeptide linked by at least one disulphide bond to a second  
 CC lipophilin-like polypeptide. Lipophilin-like protein are members of  
 CC uteroglobin superfamily. Lipophilin-like proteins are useful in the  
 CC preparation of vaccines. The complex containing lipophilin-like  
 CC proteins are useful for treating or preventing breast, ovarian or  
 CC prostate cancer. The complex is also used for determining the  
 CC presence or absence of cancer in a patient, or monitor the progress  
 CC of cancer in a patient. Lipophilin DNA is also useful in gene therapy.  
 CC The present sequence is human lipophilin B protein.

XX  
 SQ Sequence 90 AA:

Query Match 100.0%; Score 90; DB 22; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.2e-82;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAFDAPPEVAAKL 60  
 ||||||||||||||||||  
 Db 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAFDAPPEVAAKL 60

Qy 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90  
 ||||||||||||||||||  
 Db 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90

## RESULT 11

AAAB31681  
 ID AAB31681 standard; Protein: 90 AA.

XX  
 AC AAB31681;

XX  
 DT 30-APR-2001 (first entry)

XX  
 DE An endometrial specific steroid binding factor II.

XX  
 KW Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;  
 KW hESFIII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;  
 KW neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;  
 KW phagocytosis; platelet aggregation; eicosanoid; endometrial cell.

XX  
 OS Homo sapiens.

XX  
 FH Key Location/Qualifiers

XX  
 FT Peptide 1..21

XX  
 FT /note= "signal peptide"

XX  
 PN US6174992-B1.

XX  
 PD 16-JAN-2001.

XX  
 PF 08-MAR-1999; 99US-0263810.

XX  
 PR 21-MAR-1996; 96US-0014724.

XX  
 PR 21-MAR-1997; 97US-0821451.

XX  
 PA (HUMA-) HUMAN GENOME SCI INC.

XX  
 PI NI J, Yu G, Gentz R;

XX  
 DR WPI: 2001-158477/16.

XX  
 DR N-PSDB: AAF25213.

XX  
 PT New human endometrial specific steroid binding factors, useful for  
 PT treating and preventing inflammation, asthma, rhinitis, cystic  
 PT fibrosis, airway disease, neoplasia and atopy

XX  
 PS Claim 1; Fig 2; 36pp; English.

XX  
 CC The present sequence represents a human endometrial specific steroid  
 CC binding factor (hESF). The specification describes hESFI, hESFII, and  
 CC hESFIII. hESFI, II and III polypeptides, and polynucleotides encoding  
 CC them are useful for treating and preventing inflammation, asthma,  
 CC rhinitis, cystic fibrosis, airway disease, neoplasia and atopy,  
 CC inhibiting phospholipase A2 activity, binding polychlorinated  
 CC biphenyls, reducing foreign protein antigenicity, inhibiting monocyte  
 CC and neutrophil chemotaxis and phagocytosis, inhibiting platelet  
 CC aggregation, regulating eicosanoid levels in the human uterus, and for  
 CC controlling the growth of endometrial cells. hESF polypeptides and  
 CC nucleotides are also useful for research, biological, clinical or  
 CC therapeutic purposes.

XX  
 SQ Sequence 90 AA:

Query Match 100.0%; Score 90; DB 22; Length 90;

Best Local Similarity 100.0%; Pred. No. 2.2e-82;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAFDAPPEVAAKL 60  
 ||||||||||||||||||  
 Db 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAFDAPPEVAAKL 60

Qy 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90  
 ||||||||||||||||||  
 Db 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90

## RESULT 12

ABBO9634  
 ID ABB09634 standard; Protein: 90 AA.

XX  
 AC ABB09634;

XX  
 DT 29-MAY-2002 (first entry)

XX Human endometrial specific steroid-binding factor (hesf) II.  
 DE Human; endometrial specific steroid-binding factor: ESF;  
 XX prostatic steroid-binding protein; hesf I; hesf II; hesf III; asthma.  
 KM Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Reptide 1..21  
 FT /note= "signal peptide"  
 FT Protein 22..90  
 FT /note= "mature protein"  
 XX  
 XX US6338948-B1.  
 PN  
 XX  
 PD 15-JAN-2002.  
 XX  
 XX 30-MAY-2000; 2000US-0583169.  
 PF  
 XX 21-MAR-1996; 96US-01472AP.  
 PR 21-MAR-1997; 97US-0821451.  
 PR 08-MAR-1999; 99US-0263810.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 XX NI J, Yu G, Gentz R;  
 PI  
 XX WPI: 2002-215019/27.  
 DR N-PSDB; ABL41782.  
 DR  
 XX New antibody specific for human endometrial specific steroid-binding  
 PT factor (hesf) III, useful for detecting hesf III protein in biological  
 PT sample and to isolate or identify clones expressing the protein  
 PT  
 XX Disclosure; Fig 1; 36pp; English.  
 PS  
 XX The present sequence represents a endometrial specific steroid-binding  
 CC factor (hesf) II. The full length protein has a molecular weight of  
 CC 9.9 kDa. The protein has homology to rat prostatic steroid-binding  
 CC protein C2. Antibodies which bind hesf proteins, such as hesf I, hesf II,  
 CC and hesf III are useful for isolating or to identify clones expressing  
 CC the polypeptides or to purify the polypeptides by affinity  
 CC chromatography. Agonists and antagonists of hesf proteins are useful  
 CC for treating and/or preventing susceptibility to asthma.  
 CC  
 CC Sequence 90 AA:  
 SQ  
 Query Match 100.0%; Score 90; DB 23; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-82;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLIYTLALCCYQNAEFCPALVSELDFFEFISPLFKLSIAKFDAPPEAVAAKL 60  
 DB 1 MKLSVCLLIYTLALCCYQNAEFCPALVSELDFFEFISPLFKLSIAKFDAPPEAVAAKL 60  
 OY 61 GVKRCTDMSLQKRSILAEVLKILKKCSV 90  
 DB 61 GVKRCTDMSLQKRSILAEVLKILKKCSV 90

RESULT 13  
 ABB11907  
 ID ABB11907 standard; peptide; 117 AA.  
 XX  
 AC ABB11907;  
 XX  
 DT 11-JAN-2002 (first entry)  
 DE Human breast tumour-associated protein homologue, SEQ ID NO:2277.  
 XX  
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KM haematopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytosolic; osteopathic; vasotropic; cardiac; vitricide; antibacterial;  
 KW antifungal; vulnery; antitumor.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200157186-A2.  
 PN  
 XX  
 PD 09-AUG-2001.  
 XX  
 XX 05-FEB-2001; 2001WO-US03800.  
 PF  
 XX 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 PR  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX  
 XX Tang YT, Liu C, Drmanac RT;  
 PI  
 XX WPI: 2001-457740/49.  
 DR N-PSDB; ABA09151.  
 DR  
 XX Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 PT  
 XX Claim 20: Page 275; 1963pp; English.  
 PS  
 XX Sequences ABB10981-ABB12330 represent 1330 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention.

```

XX Sequence 117 AA;
SQ
Query Match 100.0%; Score 90; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.8e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60
DB 28 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 87
QY 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90
DB 88 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 117

RESULT 14
AA48606
ID AA48606 standard; Protein: 120 AA.
AC
AA48606;
DE 08-DEC-1999 (first entry)
DE Human breast tumour-associated protein 67.
KW Expressed sequence tag; EST; human; breast; cancer; gene therapy;
KW treatment; tumour; cytostatic; medicament.
XX Homo sapiens.
XX DE19813839-A1.
XX 23-SEP-1999.
XX 20-MAR-1998; 98DE-1013839.
XX 20-MAR-1998; 98DE-1013839.
XX (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
XX WPI: 1999-528981/45.
XX N-PSDB: AA233666.
XX
XX Human nucleic acid sequences and protein products from tumor breast
XX tissue, useful for breast cancer therapy -
XX
XX Claim 22: 172; 188bp; German.
XX
XX This invention describes novel human nucleic acid sequences from tumor
XX breast tissue which have cytostatic activity. The nucleic acid sequences
XX can be used to produce and isolate full-length gene sequences. They can
XX be used to express proteins, which can be used as tools to find an
XX actively against breast cancer. The sequences can be used in sense or
XX antisense form. They are especially useful for medicaments for gene
XX therapy to treat breast cancer. AA48540-Y48617 represent protein
XX fragments encoded by the expressed sequence tags described in the method
XX of the invention.
XX
SQ Sequence 120 AA;
Query Match 100.0%; Score 90; DB 20; Length 120;
Best Local Similarity 100.0%; Pred. No. 2.8e-82;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60
DB 31 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 90
QY 61 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 90

```

```

DB 91 GVKRCTDOMSLQKRSLLAEVLVKILKCSV 120

RESULT 15
AA020554
ID AA020554 standard; Protein: 89 AA.
AC
AA020554;
DE 27-JUN-2002 (first entry)
DE Protein of human lipophilin B.
DE Immunogenic epitope; hormonally regulated organ; malignant tumour;
KW Lipophilin; human.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX MISC-difference 11 /label= Lys
XX FT /note="Encoded by AGC"
XX US2002034739-A1.
XX 21-MAR-2002.
XX 07-JUL-1998; 98US-0110716.
XX 07-JUL-1998; 98US-0110716.
XX (LEHR/) LEHRER R I.
XX (ZHAO/) ZHAO C.
XX (GLAS/) GLASGOW B J.
XX
XX Lehrer RI, Zhao C, Glasgow BJ;
XX WPI: 2002-338922/37.
XX N-PSDB: AA099491.
XX
XX Peptides having the sequence of human lipophilin A, B and C are
XX associated with carcinomas of hormonally regulated organs and are
XX useful in the diagnosis and prognosis of various cancers -
XX
XX Claim 7; Fig 5; 22pp; English.
XX
XX The invention relates to a peptide comprising the amino acid sequences of
XX human lipophilin A, B, or C or its allelic variant or fragment comprising
XX at least one immunogenic epitope, which is purified and isolated, and may
XX have the N-terminal acylated and/or C-terminal amidated or be a fusion
XX protein. Molecules of the invention are used in the diagnosis and
XX prognosis of malignant tumours associated with hormonally regulated
XX organs such as uterus, ovary, prostate, testis, breast, kidney and
XX thymus. This sequence represents the human Lipophilin B protein of the
XX invention.
XX
SQ Sequence 89 AA;
Query Match 87.8%; Score 79; DB 23; Length 89;
Best Local Similarity 100.0%; Pred. No. 2.2e-71;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKGVKCTDOMSL 71
DB 11 LALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKGVKCTDOMSL 70
QY 72 QKRSLLAEVLVKILKCSV 90
DB 71 QKRSLLAEVLVKILKCSV 89

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Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:55:22 : Search time 11 Seconds

(without alignments)  
155.058 Million cell updates/sec

Title: US-09-806-301-2

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published\_Applications\_AA:\*  
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13: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB\_PEP:\*  
14: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB\_PEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	100.0	90	10	US-09-825-301-77
2	450	100.0	90	10	US-09-110-716-29
3	450	100.0	90	10	US-09-934-054-1
4	450	100.0	90	10	US-09-985-911-4
5	342	76.0	69	10	US-09-110-716-37
6	277	61.6	90	10	US-09-985-911-2
7	268	59.6	90	10	US-09-110-716-27
8	246	54.7	50	10	US-09-864-761-44240
9	238	52.9	9	9	US-09-982-598-260
10	238	52.9	83	9	US-09-989-2934-260
11	238	52.9	83	9	US-09-989-735-260
12	238	52.9	83	9	US-09-990-444-260
13	238	52.9	83	9	US-09-989-730-260
14	238	52.9	83	9	US-09-990-436-260
15	238	52.9	83	9	US-09-991-181-260
16	238	52.9	83	9	US-09-993-687-260
17	238	52.9	83	10	US-09-989-722-260
18	238	52.9	83	10	US-09-989-723-260
19	238	52.9	83	10	US-09-989-279-260

20	238	52.9	83	10	US-09-989-721-260	Sequence 260, App
21	238	52.9	83	10	US-09-989-731-260	Sequence 260, App
22	238	52.9	83	10	US-09-989-731-260	Sequence 260, App
23	238	52.9	83	10	US-09-991-071-260	Sequence 260, App
24	238	52.9	83	10	US-09-990-441-260	Sequence 260, App
25	238	52.9	83	10	US-09-991-161-260	Sequence 260, App
26	238	52.9	83	10	US-09-993-601-260	Sequence 260, App
27	238	52.9	83	10	US-09-990-451-260	Sequence 260, App
28	238	52.9	83	10	US-09-989-721-260	Sequence 260, App
29	206	45.8	11	10	US-09-934-051-5	Sequence 5, Appl1
30	202	44.9	90	10	US-09-985-911-25	Sequence 25, Appl1
31	202	44.9	90	10	US-09-985-911-25	Sequence 25, Appl1
32	172	38.2	69	10	US-09-110-715-12	Sequence 12, Appl1
33	172	38.2	69	10	US-09-110-715-36	Sequence 36, Appl1
34	171	38.0	112	10	US-09-934-051-8	Sequence 8, Appl1
35	142	31.6	74	10	US-09-110-715-35	Sequence 35, Appl1
36	111	24.7	74	10	US-09-110-715-38	Sequence 38, Appl1
37	102	22.7	91	10	US-09-934-054-9	Sequence 9, Appl1
38	91	20.2	105	10	US-09-768-826-47	Sequence 47, Appl1
39	75.5	16.8	93	9	US-10-081-817-32	Sequence 32, Appl1
40	75.5	16.8	93	12	US-10-052-586-244	Sequence 244, App
41	64.5	14.3	100	10	US-09-867-550-1430	Sequence 1430, App
42	62	13.8	178	10	US-09-969-834-1	Sequence 1, Appl1
43	59.5	13.2	95	10	US-09-925-299-1494	Sequence 1494, App
44	58	12.9	162	10	US-09-747-155-339	Sequence 339, App
45	58	12.9	226	9	US-09-895-913A-362	Sequence 362, App

#### ALIGNMENTS

RESULT 1  
US-09-825-301-77  
Sequence 77, Application US/09825301  
Patent No. US2002009738A1  
GENERAL INFORMATION:  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Dillon, David C.  
APPLICANT: Molesh, David A.  
APPLICANT: Xu, Jiangchun  
APPLICANT: Zehentner, Barbara  
APPLICANT: Persing, David H.  
TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION  
OF BREAST CANCER  
FILE REFERENCE: 210121.513  
CURRENT APPLICATION NUMBER: US/09/825,301  
CURRENT FILING DATE: 2001-04-02  
NUMBER OF SEQ ID NOS: 77  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 77  
LENGTH: 90  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-825-301-77

Query Match 100.0%; Score 450; DB 10; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1.1e-45;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFSEPLFKSLAKFPDAPPAVAKL 60  
61 GVKRCTDQMSLQKRSLLAEVLYKIKKCSV 90  
62 GVKRCTDQMSLQKRSLLAEVLYKIKKCSV 90

RESULT 2  
US-09-110-716-29  
Sequence 29, Application US/09110716A  
Patent No. US20020034739A1  
GENERAL INFORMATION:

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; APPLICANT: Lehrer, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT APPLICATION NUMBER: US/09/110,716A
; CURRENT FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Hapophilin B
US-09-110-716-29

Query Match          100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAL 60
DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAL 60
QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 3
US-09-934-054-1
; Sequence 1, Application US/09934054
; Patent No. US20020107385A1
; GENERAL INFORMATION:
; APPLICANT: Akerblom, Ingrid E.
; Hillman, Jennifer L.
; Murty, Lynn E.
; Goll, Surya K.
; Hawkins, Phillip R.
; TITLE OF INVENTION: BREAST TUMOR SPECIFIC PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025-6936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/934,054
; FILING DATE: 21-Aug-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,547
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0077 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: <unknown>
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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US-09-934-054-1

Query Match          100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAL 60
DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAL 60
QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 4
US-09-985-911-4
; Sequence 4, Application US/09985911
; Patent No. US20020151012A1
; GENERAL INFORMATION:
; APPLICANT: NI ET AL.
; TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND III
; FILE REFERENCE: P25703
; CURRENT APPLICATION NUMBER: US/09/985,911
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/583,169
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/263,810
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 08/821,451
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: 60/014,724
; PRIOR FILING DATE: 1996-03-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 90
; TYPE: PRT
; ORGANISM: human
US-09-985-911-4

Query Match          100.0%; Score 450; DB 10; Length 90;
Best Local Similarity 100.0%; Pred. No. 1,1e-45;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAL 60
DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFISPLFKLSLAKFDAPPEAVAL 60
QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 5
US-09-110-716-37
; Sequence 37, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:
; APPLICANT: Lehrer, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT APPLICATION NUMBER: US/09/110,716A
; CURRENT FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Lgmb
US-09-110-716-37

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Query Match	76.0%;	Score 342;	DB 10;	Length 69;
Best Local Similarity	100.0%;	Pred. No. 2.8e-33;		
Matches 69;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

**Oy** 22 EFCPALVSELDDEFFFI SEPLFKLSLAKFPAPPEA VAAKLGVRCTDQMSLQKRSLIAEVL 81  
**Db** 1 EFCPALVSELDDEFFFI SEPLFKLSLAKFPAPPEA VAAKLGVRCTDQMSLQKRSLIAEVL 60

QY	82	VKILKCSV	90
Db	61	VKILKCSV	69

RESULT 6  
US-09-985-911-2

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: GENERAL INFORMATION:
: APPLICANT: NI ET AL.
: TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND III
: FILING DATE: 03/25/73
: FIRM PREFERENCE: NO

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; CURRENT APPLICATION NUMBER: US/09/985,911  
 ; CURRENT FILING DATE: 2001-11-06  
 ; PRIOR APPLICATION NUMBER: 09/583,169  
 ; PRIOR FILING DATE: 2000-05-30

; PRIOR APPLICATION NUMBER: 09/263,810  
 ; PRIOR FILING DATE: 1999-03-08  
 ; PRIOR APPLICATION NUMBER: 08/821,451  
 ; PRIOR FILING DATE: 1997-03-21

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; PRIOR APPLICATION NUMBER: 60/014,724
;
; PRIOR FILING DATE: 1996-03-21
;
; NUMBER OF SEQ ID NOS: 27
;
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
;
; LENGTH: 90
;
; TYPE: PRT
;
; ORGANSISM: human
;

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Query Match	61.68;	Score 277;	DB 10;	Length 90;
Best Local Similarity	58.99;	Pred NO. 1	46-25;	

Matches	Conservative	Mismatches	Indels	Gaps
53	17	20	0	0
<p>1 MKLSVCLLLVLTALCCVQNAECPALVSELDFFFTSEPLRLSLAKFDAPPEAVAAKL 60</p>				

D5 1 MRSLVCLMWSLALCCYGAHALVCPAVASBITVFELSLDAAVNLQVAKINPPRELAATL 60

DY 61 GVKRCTDMSLQKRSLIAEVLVKILKCSV 90

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Db      61 EVKHCIDQISFKKRLSEKLVLEIVKRCGV 90

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US-09-110-716-2/  
; Sequence 27, Application US/09110716A  
; Patent No. US20020034739A1  
; GENERAL INFORMATION.

:  
 : APPLICANT: Lehrer, Robert I.  
 :  
 : APPLICANT: Zhao, Chengquan  
 :  
 : APPLICANT: Glasgow, Benjamin J.  
 :  
 : TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS

FILE REFERENCE: 22000-20596.00  
CURRENT APPLICATION NUMBER: US/09/110,716A  
CURRENT FILING DATE: 1998-07-07  
NUMBER OF SEQ ID NOS: 41

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; SOFTWARE: PALENCIN VER. 2.0
; SEQ ID NO 27
; LENGTH: 90
; TYPE: PRT
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US-09-110-716-27

Query Match	59.6%;	Score 268;	LB 10;	Length 90;
Best Local Similarity	60.2%;	Pred. No. 1.f-e-24;		
Matches	53;	Conservative	12;	Mismatches 23;
			Indels	0;
			Gaps	0;

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DB 1 MRLSVCLLLTLALCCYRANAVLQALGSEITGFLLI GKPVFEQLAKEKAPLEAAAKM 600

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QY      61 GVKRCTDQMSLQKRSLIAEVLKILKK 88  
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Db      61 EYKCCVDIMAYEKRVLTITGLGIAEKC 88
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RESULT 8  
US-09-864-761-44240

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; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K

```

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1  APPLICANT:  Chen, wensheng
2  TITLE OF INVENTION:  HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
3  TITLE OF INVENTION:  HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
4  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
5  PRT REFERENCE:  Accession: Y-1

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;; CURRENT APPLICATION NUMBER: US/09/864,765  
;; CURRENT FILING DATE: 2001-05-23  
;; PRIOR APPLICATION NUMBER: US 60/180,312  
;; PRIOR FILING DATE: 2000-02-04

;  
 ; PRIOR APPLICATION NUMBER: US 60/201,456  
 ;  
 ; PRIOR FILING DATE: 2000-05-26  
 ;  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ;  
 ; PRIOR FILING DATE: 2000-08-03  
 ;

;; PRIOR APPLICATION NUMBER: GB 24263.6  
;; PRIOR FILING DATE: 2000-10-04  
;; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PC1/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30

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 ; PRIOR APPLICATION NUMBER: US 60/234,067  
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 ; PRIOR FILING DATE: 2000-09-21  
 ;  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ;  
 ; PRIOR FILING DATE: 2000-06-30  
 ;

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;
; PRIOR FILING DATE: 2001-01-29
;
; NUMBER OF SEQ ID NOS: 49117
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; SOFTWARE: Annomax Sequence Listing Engine
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; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

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OTHER INFORMATION: MAP TO AC004127.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4

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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: AM103293.1, EVALUATE 5.00e-21
; OTHER INFORMATION: SWISSPROT HIT: O95969, EVALUATE 4.00e-22
US-09-864-761-44240

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Query Match          54.7% Score 246; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-22;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LDEFFISEPLFKLSIAKFDAPPEAVAKLGVRKCTDQMSIQKSLIAEVL 50

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RESULT 9
US-09-992-598-260
; Sequence 260, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J Christopher
; APPLICANT: Kijavlin, Ivar L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/076910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02

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; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
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; PRIOR APPLICATION NUMBER: 60/088167
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088742
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
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; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089600
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907

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Matches	45: Conservative	13: Mismatches	16: Indels	0: Gaps	0:
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Db	1	MRLSVCLLVLTALCCYQAAAEPCPALVSELLDFEFISPELFLSLAKEDAPPEAAVAKL	60		
Qy	61	GVRKCTDQMSLQK 74			
Db	61	EVKHCCTDQISFKKR 74			
RESULT	11				
	US-09-989-735-260				
	Sequence 260, Application US/09989735				
	Publication No. US20020193299A1				
	GENERAL INFORMATION:				
	APPLICANT: Ashkenazi, Avi J.				
	APPLICANT: Baker, Kevin P.				
	APPLICANT: Botstein, David				
	APPLICANT: Desnoyers, Luc				
	APPLICANT: Eaton, Dan L.				
	APPLICANT: Ferrara, Napoleone				
	APPLICANT: Fong, Sherman				
	APPLICANT: Gerber, Hanspeter				
	APPLICANT: Gerlitsen, Mary E.				
	APPLICANT: Goddard, Audrey				
	APPLICANT: Godowski, Paul J.				
	APPLICANT: Grimaldi, J. Christopher				
	APPLICANT: Grunewald, Austin L.				
	APPLICANT: Kijavlin, Ivar J.				
	APPLICANT: Napier, Mary A.				
	APPLICANT: Pan, James				
	APPLICANT: Paoni, Nicholas F.				
	APPLICANT: Ray, Margaret Ann				
	APPLICANT: Stewart, Timothy A.				
	APPLICANT: Tumas, Daniel				
	APPLICANT: Watanabe, Colin K.				
	APPLICANT: Williams, P. Mickey				
	APPLICANT: Wood, William I.				
	APPLICANT: Zhang, Zemin				
	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				
	FILE REFERENCE: P2730P1C61				
	CURRENT APPLICATION NUMBER: US/09/989,735				
	CURRENT FILING DATE: 2001-11-19				
	PRIOR APPLICATION NUMBER: 60/049787				
	PRIOR FILING DATE: 1997-06-16				
	PRIOR APPLICATION NUMBER: 60/062250				
	PRIOR FILING DATE: 1997-10-17				
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 52.9%; Score 238; DB 9; Length 83;

Best Local Similarity 60.8%; Pred. No. 4.4e-21;  
Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKLSVCLLVIALCCYQANAEFCPALVSELLDFFFISEPLFKLSLAKFDAPPEAVAAKL 60

DB 1 MKLSVCLLVIALCCYQANAEFCPALVSELLDFFFISEPLFKLSLAKFDAPPEAVAAKL 60  
QY 61 GVKRCTDOMSLQKR 74  
DB 61 EVKHCPTDQISFKR 74

## RESULT 12

US-09-990-444-260

Sequence 260, Application US/09990444

Publication No. US20020193300A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gottlieb, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavits, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

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PRIOR APPLICATION NUMBER: 60/088025

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

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PRIOR APPLICATION NUMBER: 60/088025



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? PRIOR APPLICATION NUMBER: 60/091982
? PRIOR FILING DATE: 1998-07-07
? PRIOR APPLICATION NUMBER: 60/092182
? PRIOR FILING DATE: 1998-07-09

Query Match      52.9%; Score 238; DB 9; Length 83;
Best Local Similarity 60.8%; Pred. No. 4, 4e-21;
Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY      1 MKLSVCLLVTLALCCYQANAEFCPALVSELLAEFFISEPLFKLSLAKTDAPEAVAAKL 60
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Db      1 MRLSVCLMVSLALCCYQAHALVCPAVASEITVLEFLSDAAVMIVAKLNPPEALAAKL 60
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DB 61 EVKHTDQISFKR 74

RESULT 13  
US-09-989-730-260  
Sequence 260, Application US/09989730  
Publication No. US20020197674A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertlisen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavitt, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C69  
CURRENT APPLICATION NUMBER: US/09/989,730  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/087827  
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PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 52.9%; Score 238; DB 9; Length 83;  
Best Local Similarity 60.8%; Pred. No. 4, 4e-21;  
Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKISVCLLTWLAICCYQAARFPAVSELDPEFFISEPLFKSLAKFPAPPEAVAKL 60  
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Db 1 MRLSVCLMTSLALCCQAHALWCPRVASEITVFLFLSDAAVNLQVAKLPPPALAKL 60  
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
QY 61 GVKRCTDMSLQKR 74  
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Db 61 EVKHCITDQISFKR 74  
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RESULT 14  
US-09-990-436-260  
; Sequence 260, Application US/09990436  
; Publication No. US20020198148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC14  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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; PRIOR FILING DATE: 1998-06-04  
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PRIOR APPLICATION NUMBER: 60/0919822	PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/0921822	PRIOR FILING DATE: 1998-07-09

Query Match	52.9%;	Score 238;	DB 9;	Length 83;
Best Local Similarity	60.8%;	Pred. No. 4.4e-21;		
Matches 45;	Conservative 13;	Mismatches 16;	Indels 0;	Gaps 0;

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QY 1 MKSVCLLTVLATCCYQANAERCPCALYSELIDFFFISEPLEKLSLAKFDAPPEAVAACL 60
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DB 1 MRLSVCLLWNLATCCYQAHALVCPVAASEITVLEFLSDAIVNLQVAKLNPPREALAKL 60

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QY      61 GVKRCTDQMSLQKR 74
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## RESULT 15

US-09-991-181-260  
; Sequence 260, Application US/09991181  
; Publication No. US20020197615A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC53  
; CURRENT APPLICATION NUMBER: US/09/991,181  
; PRIOR FILING DATE: 2001-11-16  
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Query Match 52.9%; Score 238; DB 9; Length 83;
Best Local Similarity 60.8%; Pred. No. 4.4e-21;
Matches 45; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELIDFFIFISEPLFKLSLAKFDAPPEVAVAL 60
Db 1 MKLSVCLLVTLALCCYQANAEFCPALVSELIDFFIFISEPLFKLSLAKFDAPPEVAVAL 60
QY 61 GVKRCTDOMSLQKR 74
Db 61 EVKHCTDQISFKKR 74

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Search completed: January 2, 2003, 14:59:08  
 Job time : 12 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 14:59:13 ; Search time 15 Seconds  
(without alignments)  
176.538 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 90  
Sequence: 1 MKLSVCLLVLTALCCYQAN.....LQKRSIAEVLKIKKCSV 90

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/prodata/1/1aa/3A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCrUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	90	100.0	90	4 US-09-263-810-4	Sequence 4, Appl1
3	90	100.0	90	4 US-08-912-276-15	Sequence 15, Appl1
4	90	100.0	90	4 US-09-583-169-4	Sequence 4, Appl1
5	90	100.0	90	4 US-09-215-818-6	Sequence 6, Appl1
6	69	76.7	69	4 US-08-912-276-23	Sequence 23, Appl1
7	45	50.0	45	4 US-08-912-276-22	Sequence 22, Appl1
8	22	24.4	22	4 US-08-912-276-21	Sequence 21, Appl1
9	15	16.7	15	4 US-08-912-276-16	Sequence 16, Appl1
10	15	16.7	15	4 US-08-912-276-17	Sequence 17, Appl1
11	15	16.7	16	4 US-08-912-276-18	Sequence 18, Appl1
12	15	16.7	16	4 US-08-912-276-20	Sequence 20, Appl1
13	15	16.7	16	4 US-08-912-276-19	Sequence 19, Appl1
14	8	8.9	90	3 US-08-821-451A-2	Sequence 2, Appl1
15	8	8.9	90	4 US-09-263-810-2	Sequence 2, Appl1
16	8	8.9	90	4 US-09-583-169-2	Sequence 2, Appl1
17	8	8.9	91	1 US-08-455-896-8	Sequence 8, Appl1
18	8	8.9	91	2 US-08-933-149-8	Sequence 8, Appl1
19	8	8.9	91	2 US-09-082-343-8	Sequence 8, Appl1
20	8	8.9	91	2 US-09-082-253-8	Sequence 8, Appl1
21	8	8.9	91	5 PCr-US96-08235-8	Sequence 8, Appl1
22	7	7.8	190	4 US-09-134-001C-3138	Sequence 3138, Ap
23	7	7.8	223	2 US-08-869-793-6	Sequence 6, Appl1
24	7	7.8	224	1 US-08-287-959-6	Sequence 6, Appl1
25	7	7.8	570	3 US-08-826-246-2	Sequence 2, Appl1
26	7	7.8	570	3 US-08-944-495-2	Sequence 2, Appl1
27	7	7.8	570	3 US-09-126-640-7	Sequence 7, Appl1

28	7	7.8	570	4 US-08-925-588-2	Sequence 2, Appl1
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30	7	7.8	648	4 US-09-183-706-43	Sequence 43, Appl1
31	7	7.8	648	4 US-09-567-995-43	Sequence 43, Appl1
32	7	7.8	2101	1 US-08-466-390-4	Sequence 4, Appl1
33	7	7.8	2101	1 US-08-470-950-4	Sequence 4, Appl1
34	7	7.8	2101	1 US-08-467-781-4	Sequence 4, Appl1
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38	7	7.8	2101	5 PCr-US93-06160-4	Sequence 4, Appl1
39	7	7.8	3079	5 PCr-US94-00190-4	Sequence 4, Appl1
40	6	6.7	13	1 US-08-465-325-135	Sequence 135, App
41	6	6.7	13	4 US-09-115-737-135	Sequence 135, App
42	6	6.7	21	1 US-07-965-663A-1	Sequence 1, Appl1
43	6	6.7	21	1 US-07-965-663A-22	Sequence 22, Appl1
44	6	6.7	22	1 US-07-965-663A-4	Sequence 4, Appl1
45	6	6.7	22	1 US-07-965-663A-20	Sequence 20, Appl1

## ALIGNMENTS

RESULT 1  
US-08-821-451A-4  
; Sequence 4, Application US/08821451A  
; Patent No. 6066724  
; GENERAL INFORMATION:  
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz  
; TITLE OF INVENTION: Human Endometrial Specific Steroid-  
; TITLE OF INVENTION: Binding Factor I, II and III  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/821,451A  
; FILING DATE: March 21, 1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/014,724  
; FILING DATE: March 21, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-521 (PR257)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1744  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 90 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-821-451A-4  
Query Match 100.0%; Score 90; DB 3; Length 90;  
Best Local Similarity 100.0%; Pred. No. 3.4e-80;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLSVCLLVLTALCCYQANAEPCPALVSELDPEFFISEPLFKLSLAKFPAPPAEVAAKL 60

|||||  
Db 1 MRLSVCLLVTLALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60  
OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
|||||  
Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 2  
US-09-263-810-4  
; Sequence 4, Application US/09263810  
; Patent No. 6174992  
; GENERAL INFORMATION:  
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz  
; TITLE OF INVENTION: Human Endometrial Specific Steroid-  
; TITLE OF INVENTION: Binding Factor I, II and III  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,810  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/821,451  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 90 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-09-263-810-4

Query Match 100.0%; Score 90; DB 4; Length 90;  
Best Local Similarity 100.0%; Pred. No. 3.4e-80;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRLSVCLLVTLALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60  
|||||  
Db 1 MRLSVCLLVTLALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60  
OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
|||||  
Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 3  
US-08-912-276-15  
; Sequence 15, Application US/08912276  
; Patent No. 6183952  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A.  
; APPLICANT: Cohen, Maurice

APPLICANT: Colpits, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Gordon, Julian  
APPLICANT: Granados, Edward N.  
APPLICANT: Hodges, Steven C.  
APPLICANT: Klass, Michael R.  
APPLICANT: Kratochvil, Jon D.  
APPLICANT: Roberts-Rapp, Lisa  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6183952e  
US-08-912-276-15

Query Match 100.0%; Score 90; DB 4; Length 90;  
Best Local Similarity 100.0%; Pred. No. 3.4e-80;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRLSVCLLVTLALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60  
|||||  
Db 1 MRLSVCLLVTLALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60  
OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
|||||  
Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 4  
US-09-583-169-4  
; Sequence 4, Application US/09583169  
; Patent No. 6338948  
; GENERAL INFORMATION:  
; APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz  
; TITLE OF INVENTION: Human Endometrial Specific Steroid-  
; TITLE OF INVENTION: Binding Factor I, II and III  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,



```

ADDRESSER: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,169
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-583-169-4

Query Match          100.0%; Score 90; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.4e-80;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPEAAVAAKL 60
DB 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPEAAVAAKL 60

QY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90
DB 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90

RESULT 5
US-09-215-818-6
Sequence 6, Application US/09215818A
Patent No. 6379671
GENERAL INFORMATION:
APPLICANT: Colpitts, Tracey
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
FILE REFERENCE: 5972.US.P2
CURRENT APPLICATION NUMBER: US/09/215,818A
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 08/912,276
EARLIER FILING DATE: 1997-08-17
EARLIER APPLICATION NUMBER: 08/697,105
EARLIER FILING DATE: 1996-08-19
EARLIER APPLICATION NUMBER: 08/912,149
EARLIER FILING DATE: 1997-08-15
EARLIER APPLICATION NUMBER: 08/697,106
EARLIER FILING DATE: 1996-08-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 90
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-215-818-6
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Query Match          100.0%; Score 90; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.4e-80;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPEAAVAAKL 60
DB 1 MKLSVCLLVLTALCCYQNAEPCPALVSELDFFFI SEPLFKLSLAKDPAPPEAAVAAKL 60

QY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90
DB 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSY 90

RESULT 6
US-08-912-276-23
Sequence 23, Application US/08912276
Patent No. 6183952
GENERAL INFORMATION:
APPLICANT: Billing-Medel, Patricia A.
APPLICANT: Cohen, Maurice
APPLICANT: Colpitts, Tracey L.
APPLICANT: Friedman, Paula N.
APPLICANT: Gordon, Julian
APPLICANT: Granados, Edward N.
APPLICANT: Hodges, Steven C.
APPLICANT: Klass, Michael R.
APPLICANT: Kratochvil, Jon D.
APPLICANT: Roberts-Rapp, Lisa
APPLICANT: Russell, John C.
APPLICANT: Stroupe, Steven D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,276
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5972.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: NO. 6183952e
US-08-912-276-23

Query Match          76.7%; Score 69; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 6.2e-60;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 22 EECPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKLGVRCTDOMSLQKRSILAEVL 81  
|||||  
Db 1 EECPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKLGVRCTDOMSLQKRSILAEVL 60  
Oy 82 VKILKCSV 90  
|||||  
Db 61 VKILKCSV 69

## RESULT 7

US-08-912-276-22  
; Sequence 22, Application US/08912276  
; Patent No. 6183952  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A.  
; APPLICANT: Cohen, Maurice  
; APPLICANT: Colpits, Tracey L.  
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Gordon, Julian  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klass, Michael R.  
; APPLICANT: Kratochvil, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa  
; APPLICANT: Russell, John C.  
; APPLICANT: Stroupe, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912.276  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5972. US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 45 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6183952e  
US-08-912-276-22

Query Match 50.0%; Score 45; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 7.9e-37;  
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 46 LAKFDAPPEAVAAKLGVRCTDOMSLQKRSILAEVLVKILKCSV 90  
|||||  
Db 1 LAKFDAPPEAVAAKLGVRCTDOMSLQKRSILAEVLVKILKCSV 45

## RESULT 8

US-08-912-276-21  
; Sequence 21, Application US/08912276  
; Patent No. 6183952  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A.  
; APPLICANT: Cohen, Maurice  
; APPLICANT: Colpits, Tracey L.  
; APPLICANT: Friedman, Paula N.  
; APPLICANT: Gordon, Julian  
; APPLICANT: Granados, Edward N.  
; APPLICANT: Hodges, Steven C.  
; APPLICANT: Klass, Michael R.  
; APPLICANT: Kratochvil, Jon D.  
; APPLICANT: Roberts-Rapp, Lisa  
; APPLICANT: Russell, John C.  
; APPLICANT: Stroupe, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/912.276  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Becker, Cheryl L.  
; REGISTRATION NUMBER: 35,441  
; REFERENCE/DOCKET NUMBER: 5972. US.P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 847/935-1729  
; TELEFAX: 847/938-2623  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6183952e  
US-08-912-276-21

Query Match 24.4%; Score 22; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 8.6e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 69 MSLOKRSILAEVLVKILKCSV 90  
|||||  
Db 1 MSLOKRSILAEVLVKILKCSV 22

## RESULT 9

US-08-912-276-16  
; Sequence 16, Application US/08912276  
; Patent No. 6183952  
; GENERAL INFORMATION:  
; APPLICANT: Billing-Medel, Patricia A.

```

? APPLICANT: Cohen, Maurice
? APPLICANT: Colpitts, Tracey L.
? APPLICANT: Friedman, Paula N.
? APPLICANT: Gordon, Julian
? APPLICANT: Granados, Edward N.
? APPLICANT: Hodges, Steven C.
? APPLICANT: Klass, Michael R.
? APPLICANT: Kratochvill, Jon D.
? APPLICANT: Roberts-Rapp, Lisa
? APPLICANT: Russell, John C.
? APPLICANT: Stroupe, Steven D.
? TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
? TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
? NUMBER OF SEQUENCES: 25
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/912,276
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Becker, Cheryl L
? REGISTRATION NUMBER: 35,441
? REFERENCE/DOCKET NUMBER: 5972.US.P1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847/935-1729
? TELEFAX: 847/938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 16:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: NO. 6183952e
? US-08-912-276-16

Query Match 16.7%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 EFCPALVSELDPEFF 36
DB 1 EFCPALVSELDPEFF 15

RESULT 10
US-08-912-276-19
? Sequence 19, Application US/08912276
? Patent No. 6183952
? GENERAL INFORMATION:
? APPLICANT: Billing-Medel, Patricia A.
? APPLICANT: Cohen, Maurice
? APPLICANT: Colpitts, Tracey L.
? APPLICANT: Friedman, Paula N.
? APPLICANT: Gordon, Julian
? APPLICANT: Granados, Edward N.
? APPLICANT: Hodges, Steven C.
? APPLICANT: Klass, Michael R.
? APPLICANT: Kratochvill, Jon D.
```

```

? APPLICANT: Roberts-Rapp, Lisa
? APPLICANT: Russell, John C.
? APPLICANT: Stroupe, Steven D.
? TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
? TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
? NUMBER OF SEQUENCES: 25
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
? STREET: 100 Abbott Park Road
? CITY: Abbott Park
? STATE: IL
? COUNTRY: USA
? ZIP: 60064-3500
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/912,276
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Becker, Cheryl L
? REGISTRATION NUMBER: 35,441
? REFERENCE/DOCKET NUMBER: 5972.US.P1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 847/935-1729
? TELEFAX: 847/938-2623
? TELEX:
? INFORMATION FOR SEQ ID NO: 19:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: NO. 6183952e
? US-08-912-276-19

Query Match 16.7%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 54 EAVAAKLGVRCTDQ 68
DB 1 EAVAAKLGVRCTDQ 15

RESULT 11
US-08-912-276-17
? Sequence 17, Application US/08912276
? Patent No. 6183952
? GENERAL INFORMATION:
? APPLICANT: Billing-Medel, Patricia A.
? APPLICANT: Cohen, Maurice
? APPLICANT: Colpitts, Tracey L.
? APPLICANT: Friedman, Paula N.
? APPLICANT: Gordon, Julian
? APPLICANT: Granados, Edward N.
? APPLICANT: Hodges, Steven C.
? APPLICANT: Klass, Michael R.
? APPLICANT: Kratochvill, Jon D.
? APPLICANT: Roberts-Rapp, Lisa
? APPLICANT: Russell, John C.
? APPLICANT: Stroupe, Steven D.
? TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
? TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST
? NUMBER OF SEQUENCES: 25
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Abbott Laboratories
```

STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 6183952e  
US-08-912-276-17

Query Match 16.7%; Score 15; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 ISEPLFKLSLAKFDA 51  
DB 1 ISEPLFKLSLAKFDA 15

RESULT 12  
US-08-912-276-18  
Sequence 18, Application US/08912276  
Patent No. 6183952  
GENERAL INFORMATION:  
APPLICANT: Billing-Medel, Patricia A.  
APPLICANT: Cohen, Maurice  
APPLICANT: Colpitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Gordon, Julian  
APPLICANT: Granados, Edward N.  
APPLICANT: Hodges, Steven C.  
APPLICANT: Klass, Michael R.  
APPLICANT: Kratochvil, Jon D.  
APPLICANT: Roberts-Rapp, Lisa  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 6183952e  
US-08-912-276-18

Query Match 16.7%; Score 15; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 SLAKFDAPPEAVNAK 59  
DB 1 SLAKFDAPPEAVNAK 15

RESULT 13  
US-08-912-276-20  
Sequence 20, Application US/08912276  
Patent No. 6183952  
GENERAL INFORMATION:  
APPLICANT: Billing-Medel, Patricia A.  
APPLICANT: Cohen, Maurice  
APPLICANT: Colpitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Gordon, Julian  
APPLICANT: Granados, Edward N.  
APPLICANT: Hodges, Steven C.  
APPLICANT: Klass, Michael R.  
APPLICANT: Kratochvil, Jon D.  
APPLICANT: Roberts-Rapp, Lisa  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Steven D.  
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

\* FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972.US.P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6183952e  
US-08-912-276-20

Query Match 16.7%; Score 15; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 69 MSLSKRSLSIAEVLVK 83  
|||||  
Db 1 MSLSKRSLSIAEVLVK 15

RESULT 14  
US-08-821-451A-2  
Sequence 2, Application US/08821451A  
Patent No. 6066724  
GENERAL INFORMATION:  
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-  
TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/821,451A  
FILING DATE: March 21, 1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/014,724  
FILING DATE: March 21, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-821-451A-2

Query Match 8.9%; Score 8; DB 3; Length 90;

Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYQA 19  
|||||  
Db 12 LALCCYQA 19

RESULT 15  
US-09-263-810-2  
Sequence 2, Application US/09263810  
Patent No. 6174992  
GENERAL INFORMATION:  
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-  
TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/263,810  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/821,451  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-263-810-2

Query Match 8.9%; Score 8; DB 4; Length 90;  
Best Local Similarity 100.0%; Pred. No. 1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYQA 19  
|||||  
Db 12 LALCCYQA 19

Search completed: January 2, 2003, 15:01:30  
JOD time : 16 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:56:08 : Search time 13 Seconds  
(without alignments)  
287.144 Million cell updates/sec

Title: US-09-806-301-2  
Perfect score: 90  
Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLVKKCSV 90

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476320 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	90	1 LPPB_HUMAN	O95969 homo sapien
2	8	8.9	91	1 UTER_HUMAN	P11684 homo sapien
3	8	8.9	112	1 PSC2_RAT	P02781 rattus norv
4	8	8.9	279	1 SPBP_RAT	P08723 rattus norv
5	7	7.8	90	1 LPPA_HUMAN	O95968 homo sapien
6	7	7.8	141	1 HBA_BALAC	P18971 balenopter
7	7	7.8	141	1 HBA_CERSI	P01963 ceratotheri
8	7	7.8	141	1 HBA_ERIEU	P01949 erinaceus e
9	7	7.8	141	1 HBA_RH1UN	P09906 rhinoceros
10	7	7.8	141	1 HBA_TAPTE	P01962 tapirus ter
11	7	7.8	141	1 HBA_TURTR	P18978 turists tr
12	7	7.8	168	1 YBPQ_BACSU	P54158 bacillus su
13	7	7.8	177	1 YG09_SYNY3	P73844 synchocyst
14	7	7.8	248	1 PCRB_METTH	O26652 methanobact
15	7	7.8	328	1 LAID_ECOLI	P76316 escherichia
16	7	7.8	339	1 CWC2_YEAST	O12046 saccharomyc
17	7	7.8	344	1 STSY_RAUSE	P15324 raouvolifila s
18	7	7.8	352	1 RNPD_ECO57	P58335 escherichia
19	7	7.8	352	1 RNPD_ECOLI	P76182 escherichia
20	7	7.8	424	1 YG5Y_YEAST	O53329 saccharomyc
21	7	7.8	431	1 NOOE_THETH	O56229 thecmarus the
22	7	7.8	453	1 NH12_CABEL	O21701 caenorhabdl
23	7	7.8	470	1 SNXH_HUMAN	O15036 homo sapien
24	7	7.8	683	1 LCFE_HUMAN	O90155 homo sapien
25	7	7.8	3079	1 ITR2_YEAST	P19158 saccharomyc
26	6	6.7	34	1 ITR2_MOMCO	P82409 momordica c
27	6	6.7	44	1 YCRC_MYCCA	P45620 mycoplasma
28	6	6.7	73	1 RCRO_BPD3	O37907 bacteriophag
29	6	6.7	91	1 UTER_LBPRA	P06913 lepus capen
30	6	6.7	91	1 UTER_RABIT	P02779 oryctolagus
31	6	6.7	99	1 NEUY_DICLA	P09140 dicentrarch
32	6	6.7	112	1 YQXA_BACSU	P38425 bacillus su
33	6	6.7	113	1 DHSD_COXBU	P51057 coxiella bu

34	6	6.7	114	1 YFEC_ECOLI	P27239 escherichia
35	6	6.7	129	1 RECA_BACTN	O45791 bacterioides
36	6	6.7	129	1 VDBP_CAMVC	P03552 cauliflower
37	6	6.7	129	1 VDBP_CAMVE	O02967 cauliflower
38	6	6.7	129	1 VDBP_CAMVN	O00967 cauliflower
39	6	6.7	134	1 YTKC_BACSU	O34863 bacillus su
40	6	6.7	140	1 HBA_TRAST	P04237 tragelaphus
41	6	6.7	141	1 HBA_ARCGA	P41329 arctoccephal
42	6	6.7	141	1 HBAI_BOSMU	P01967 bos mutus g
43	6	6.7	141	1 HBAI_BUBBU	O91507 bubalus bub
44	6	6.7	141	1 HBAI_GALCR	P14239 galago cras
45	6	6.7	141	1 HBAI_HYLLA	O91535 hylobates 1

## ALIGNMENTS

RESULT 1	ID	LPBP_HUMAN	STANDARD:	PRT:	90 AA.
AC	O95969:				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Lipophilin B precursor (Secretoglobin family 1D member 2).				
GN	SCGB1D2 OR LIPHB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99167354; PubMed=10066439;				
RA	Zhao C., Nguyen T., Yusifov T., Glasgow H.J., Lehrer R.I.;				
RT	"Lipophilins: human peptides homologous to rat prostatein.";				
RL	Biochem. Biophys. Res. Commun. 256:147-155(1999).				
CC	-1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND				
CC	ESTRADIOL, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.				
CC	MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.				
CC	-1- SUBCELLULAR LOCATION: Secreted (Potential).				
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION WAS FOUND IN SKELETAL				
CC	MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID				
CC	RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY),				
CC	AND SALIVARY GLAND.				
CC	-1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN				
CC	SUBFAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).				
CC	-----				
DR	EMBL: AJ224172; CA11864.1; -				
DR	Genew: HGNC:18396; SCGB1D2.				
DR	InterPro: IPR000329; Uterogloblin.				
DR	Pfam: PF01099; Uterogloblin; 1.				
DR	PRINTS: PR00486; UTEROGLOBIN.				
DR	SMART: SM00096; UTS; 1.				
KW	Signal.				
FT	SIGNAL 1 21				POTENTIAL.
FT	CHAIN 22 90				LIPOPHILIN B.
SQ	SEQUENCE 90 AA; 9925 MW; 17BB555ED015D1AF CRC64;				
QY	1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFTSEPLFKLSLAKFPAPRAVAKL 60				
DB	1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFTSEPLFKLSLAKFPAPRAVAKL 60				

OY 61 GVKRCTDQMSLOKRSIAEVLVILKRCV 90  
 DB 61 GVKRCTDQMSLOKRSIAEVLVILKRCV 90

RESULT 2  
 UTER\_HUMAN STANDARD: PRT: 91 AA.  
 ID UTER\_HUMAN STANDARD: PRT: 91 AA.  
 AC P1684: Q9UCM4: Q9UCM2:  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Clara cell phospholipid-binding protein precursor (CCBP) (Clara cells  
 DE 10 kDa secretory protein) (CC10) (Uteroglobin) (Urine protein 1)  
 DE (UPI).  
 GN SCGB1A1 OR UGB OR CC10 OR CCSP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=89000784; PubMed=3167058;  
 RA Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L.,  
 RA Anthony J., Squeglia N.;  
 RT "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa  
 RT protein.";  
 RL Biochim. Biophys. Acta 950:329-337(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=95250987; PubMed=7733299;  
 RA Hay J.G., Daniel C., Chu C., Crystal R.G.;  
 RT "Human CC10 gene expression in airway epithelium and subchromosomal  
 RT locus suggest linkage to airway disease.";  
 RL Am. J. Physiol. 268:L565-L575(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-18 FROM N.A.  
 RX MEDLINE=93350776; PubMed=1284526;  
 RA Wolf M., Kug J., Hackenberg R., Gessler M., Grzeschik K.-H.,  
 RA Beato M., Suske G.;  
 RT "Human CC10, the homologue of rabbit uteroglobin: genomic cloning,  
 RT chromosomal localization and expression in endometrial cell lines.";  
 RL Hum. Mol. Genet. 1:371-378(1992).  
 RN [5]  
 RP SEQUENCE OF 22-74.  
 RC TISSUE-Urine;  
 RX MEDLINE=93016476; PubMed=1400743;  
 RA Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;  
 RT "Simple and high-yield purification of urine protein 1 using  
 RT immunofluorescence chromatography: evidence for the identity of urine  
 RT protein 1 and human Clara cell 10-kilodalton protein.";  
 RL J. Chromatogr. A 577:25-35(1992).  
 RN [6]  
 RP SEQUENCE OF 22-45.  
 RC TISSUE-Urine;  
 RX MEDLINE=93009001; PubMed=1395029;  
 RA Bernard A., Roels H., Lauwers R., Witters R., Gielens C.,  
 RA Soumilion A., Van Damme J., De Ley M.;  
 RT "Human urinary protein 1: evidence for identity with the Clara cell  
 RT protein and occurrence in respiratory tract and urogenital  
 RT secretions.";  
 RL Clin. Chim. Acta 207:239-249(1992).  
 RN [7]  
 RP SEQUENCE OF 22-33.  
 RX MEDLINE=21648993; PubMed=11788998;

RA Chatfouri B., Stahlbom B., Tagesson C., Lindahl M.;  
 RT "Newly identified proteins in human nasal lavage fluid from  
 RT non-smokers and smokers using two-dimensional gel electrophoresis and  
 RT peptide mass fingerprinting.";  
 RL Proteomics 2:112-120(2002).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95393197; PubMed=7664082;  
 RA Umland T.C., Swaminathan S., Singh G., Warty V., Furey W.,  
 RA Fletcher J., Sax M.;  
 RT "Structure of a human Clara cell phospholipid-binding protein-11-glycine  
 RT complex at 1.9-A resolution.";  
 RL Nat. Struct. Biol. 1:538-545(1994).  
 CC -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,  
 CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT  
 CC INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.  
 CC -1- TISSUE SPECIFICITY: CLARA CELLS (NONCILIATED CELLS OF THE  
 CC SURFACE EPITHELIUM OF THE PULMONARY AIRWAYS).  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLIBIN FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----

DR EMBL: X13197; CAA31584.1; -  
 DR EMBL: U01101; AAA81885.1; -  
 DR EMBL: U01102; AAA18297.1; -  
 DR EMBL: BC004481; AAA04481.1; -  
 DR EMBL: X59875; CAA42532.1; -  
 DR PIR: J50036; JS0036.  
 DR PIR: S26651; S26651.  
 DR HSP: P02779; 10TG.  
 DR GeneW: HGNC:12523; SCGB1A1.  
 DR MIM: 192020; -  
 DR InterPro: IPR003628; Uteroglibn.sub.  
 DR InterPro: IPR000329; Uteroglibin.  
 DR Pfam: PF01099; Uteroglibin; 1.  
 DR PRINTS: PR00486; UTEROGLIBIN.  
 DR PRODOM: PD012475; Uteroglibn\_sub; 1.  
 DR SMART: SM00096; UTG; 1.  
 DR PROSITE: PS00403; UTEROGLIBIN\_1; 1.  
 DR PROSITE: PS00404; UTEROGLIBIN\_2; 1.  
 KW Phospholipase A2 inhibitor; Signal; Polymorphism.  
 FT SIGNAL 1 21  
 FT CHAIN 22 91 CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.  
 FT DISULFID 24 24 INTERCHAIN (WITH C-90').  
 FT DISULFID 90 90 INTERCHAIN (WITH C-24').  
 FT VARIANT 56 56 R -> G (IN DBSNP:1802634).  
 FT VARIANT 68 68 /FTID-VAR\_012045.  
 FT VARIANT 68 68 T -> A (IN DBSNP:1802632).  
 FT VARIANT 68 68 /FTID-VAR\_012046.  
 FT CONFLICT 24 24 C -> E (IN REF. 7).  
 FT SEQUENCE 91 AA; 9994 MW; FE65ACA678F12ABD CRC64;

Query Match 8.9%; Score 8; DB 1; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 0.48;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 LVTALCC 16  
 DB 9 LVTALCC 16

RESULT 3  
 ID PSC2\_RAT STANDARD: PRT: 112 AA.  
 AC P02781;  
 DT 21-JUL-1986 (Rel. 01, Created)



DT 01-JAN-1988 (Rel. 06, last sequence update)  
 DT 30-MAY-2000 (Rel. 39, last annotation update)  
 DE Prostatic steroid-binding protein C2 chain precursor (Prostatein  
 DE peptide C2).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBITaxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87146484; PubMed=2881277;  
 RA Delaney B., Dittck L., Decourt J.-L., Claessens F., Peeters B.,  
 RA Rombaux W.;  
 RT "Rat prostatic binding protein: the complete sequence of the C2 gene  
 RT and its flanking regions";  
 RL Nucleic Acids Res. 15:1627-1641(1987).  
 RN [2]  
 RP SEQUENCE OF 21-112.  
 RX MEDLINE=83209619; PubMed=6343081;  
 RA Peeters B., Heyns W., Mous J., Rombaux W.;  
 RT "Structural studies on rat prostatic binding protein. The primary  
 RT structure of component C2 from subunit S.";  
 RL Eur. J. Biochem. 132:669-679(1983).  
 RN [3]  
 RP SEQUENCE OF 1-100 FROM N.A.  
 RX MEDLINE=82220075; PubMed=6896362;  
 RA Parker M., Needham M., White R.;  
 RT "Prostatic steroid binding protein: gene duplication and steroid  
 RT binding.";  
 RL Nature 298:92-94(1982).  
 CC -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY  
 CC GLYCOPROTEIN OF VENTRAL PROSTATE GLAND.  
 CC -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED  
 CC C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)  
 CC HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC  
 CC (C1:C3/C3:C2) PROSTATEIN MOLECULES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: LINKED BY THREE DISULFIDE BONDS TO C3.  
 CC -1- MISCELLANEOUS: THE HETERODIMER CAN BIND NON-POLAR STEROIDS,  
 CC CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN  
 CC SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X05034; CAA28708.1; -;  
 DR EMBL: V01256; CAA24569.1; -;  
 DR EMBL: J00776; AAA51641.1; -;  
 DR PIR: A03251; BORT2.  
 DR PIR: A26671; A26671.  
 DR InterPro: IPR000329; Uteroglobln.  
 DR PROSITE: PS00403; UTEROGLOBIN\_1; FALSE\_NEG.  
 DR PROSITE: PS00404; UTEROGLOBIN\_2; FALSE\_NEG.  
 KW Steroid-binding; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 112  
 FT MOD\_RES 21 21  
 FT DISULFID 28 28  
 FT DISULFID 69 69  
 FT DISULFID 92 92  
 FT CONFLICT 26 26  
 FT CONFLICT 88 88  
 FT CONFLICT 96 96  
 FT SEQUENCE 112 AA; 12828 MW; DA65A6A82E677864 CRC64;  
 Query Match 8.9%; Score 8; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 0.57;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 49 FDPAPPEAV 56  
 DB 53 FDPAPPEAV 60  
 ID SPBP\_RAT STANDARD; PRT; 279 AA.  
 AC P08723;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Prostatic spermine-binding protein precursor (SBP).  
 GN SBP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NC NCBITaxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87137538; PubMed=3818623;  
 RA Chang C., Saltzman A.G., Hlipakka R.A., Huang I.-Y., Liao S.;  
 RT "Prostatic spermine-binding protein. Cloning and nucleotide sequence  
 RT of cDNA, amino acid sequence, and androgenic control of mRNA level.";  
 RL J. Biol. Chem. 263:2826-2831(1987).  
 RN [2]  
 RP SEQUENCE, AND REVISIONS.  
 RX MEDLINE=89000602; PubMed=3166977;  
 RA Anderegg R.J., Carr S.A., Huang I.-Y., Hlipakka R.A., Chang C.,  
 RA Liao S.;  
 RT "Correction of the cDNA-derived protein sequence of prostatic  
 RT spermine binding protein: pivotal role of tandem mass spectrometry in  
 RT sequence analysis.";  
 RL Biochemistry 27:4214-4221(1988).  
 CC -1- FUNCTION: SPERMINE-BINDING PROTEIN IS AN ANDROGEN REGULATED  
 CC VENTRAL PROSTATE GLYCOPROTEIN THAT BINDS VARIOUS POLYAMINES.  
 CC -1- TISSUE SPECIFICITY: PROSTATE.  
 CC -1- SIMILARITY: TO MOOSE SBP.  
 CC -----  
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 CC -----  
 DR EMBL: J02675; AAA2113.1; ALT\_SEQ.  
 DR PIR: A29561; A29561.  
 DR PIR: A28714; A28714.  
 DR InterPro: IPR001229; Jacalin\_lectin.  
 DR Pfam: PF01419; Jacalin; 1.  
 KW Glycoprotein; Signal.  
 FT SIGNAL 1 17  
 FT CHAIN 18 279  
 FT MOD\_RES 18 18  
 FT CARBOHYD 62 62  
 FT DOMAIN 154 279  
 FT SEQUENCE 279 AA; 31080 MW; 3BED01A02517A65 CRC64;  
 Query Match 8.9%; Score 8; D3 1; Length 279;  
 Best Local Similarity 100.0%; Pred. No. 1.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LLVVTAL 14  
 DB 2 LLVVTAL 9  
 RESULT 5

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LPPA_HUMAN
ID LPPA_HUMAN STANDARD: PRT: 90 AA.
AC 095968;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lipophilin A precursor (Secretoglobin family 1D member 1).
GN SCGB1D1 OR LIPHA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99167354; PubMed=10066439;
RA Zhao C., Nguyen T., Yusifov T., Glasgow B.J., Lehrer R.I.;
RT "Lipophilins: human peptides homologous to rat prostatein.";
RL Biochem. Biophys. Res. Commun. 256:147-155(1999).
RN [2]
RP SEQUENCE OF 22-90, AND MASS SPECTROMETRY.
RX MEDLINE=98385871; PubMed=9720917;
RA Lehrer R.I., Xu G., Abduragimov A., Dinh N.N., Qu X.-D., Martin D.,
RA Glasgow B.J.;
RT "Lipophilin, a novel heterodimeric protein of human tears.";
RL FEBS Lett. 433:163-167(1998).
CC -1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS. MAY ALSO BIND
CC ESTRADIOL, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.
CC MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
CC -1- SUBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C
CC (MAMMALOBLIN B) MONOMER ASSOCIATED HEAD TO HEAD.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN LACHRYMAL GLAND, THYMUS, KIDNEY,
CC TESTIS, OVARY AND SALIVARY GLAND.
CC -1- MASS SPECTROMETRY: MW=7574.69; METHOD=Electrospray; RANGE=22-90.
CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AJ224171; CA11863.1; -
DR Genew; HGNC:18395; SCGB1D1.
DR InterPro: IPR000329; uteroglobln.
DR Pfam: PF01099; uteroglobln; 1.
DR PRINTS: PR00486; UTEROGLOBIN.
DR SMART: SM00096; UTG; 1.
DR KMW
DR SIGNAL
FT CHAIN 1 21 LIPOPHILIN A.
FT SIGNAL 90
SQ SEQUENCE 90 AA: 9898 MW: DE2DAF7565A87D34 CRC64:
Query Match 7.8%; Score 7; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 LSVCLL 9
DB 3 LSVCLL 9
RESULT 6
HBA_BALAC STANDARD: PRT: 141 AA.
ID HBA_BALAC
AC P18971;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin alpha chain.

```

```

GN HBA.
OS Balenoptera acutorostrata (Minke whale) (Lesser rorqual).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balenopteridae; Balenoptera.
OX NCBI_Taxid=9767;
RN [1]
RP SEQUENCE.
RA Abbaal A., Rucknagel P., Matsuda G., Zaidi Z.H., Braunitzer G.;
RT "The primary structure of Minke-whale (Balenoptera acutorostrata -
RT Cetacea) hemoglobin.";
RL J. Chem. Soc. Pak. 6:253-256(1984).
CC -1- FUNCTION: INVOLVED IN OXYGEN TRANSPORT FROM THE LUNG TO THE
CC VARIOUS PERIPHERAL TISSUES.
CC -1- SUBUNIT: Heterotrimer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: RED BLOOD CELLS.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: S06520; HAHMK.
DR HSSP: P01922; 1B20.
DR InterPro: IPR002338; Alpha_haem.
DR Pfam: PF00042; globln; 1.
DR PRINTS: PR00612; ALPHAHAEW.
DR PROSITE: PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport; Erythrocyte;
KW Polymorphism.
FT METAL 58 58 IRON (HEME DISTAL LIGAND).
FT METAL 87 87 IRON (HEME PROXIMAL LIGAND).
FT VARIANT 21 21 G -> S.
FT VARIANT 96 96 A -> V.
SQ SEQUENCE 141 AA: 15406 MW: 0B0C26CDF7B72B53 CRC64:
Query Match 7.8%; Score 7; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LVTTLAL 14
DB 105 LVTTLAL 111
RESULT 7
HBA_CERST STANDARD: PRT: 141 AA.
ID HBA_CERST
AC P01963;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hemoglobin alpha chain.
GN HBA.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_Taxid=9807;
RN [1]
RP SEQUENCE.
RX MEDLINE=83055102; PubMed=7141412;
RA Mazur G., Braunitzer G., Wright P.G.;
RT "The primary structure of the hemoglobin from a white rhinoceros
RT (Ceratotherium simum, perissodactyla): beta 2 Glu.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1077-1085(1982).
CC -1- FUNCTION: Involved in oxygen transport from the lung to the
CC various peripheral tissues.
CC -1- SUBUNIT: Heterotrimer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: Red blood cells.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.
DR PIR: A02286; HARNW.
DR HSSP: P01958; 2MBH.
DR InterPro: IPR002338; Alpha_haem.
DR Pfam: PF00042; globln; 1.
DR PRINTS: PR00612; ALPHAHAEW.
DR PROSITE: PS01033; GLOBIN; 1.

```

KW Heme; Oxygen transport; Transport; Erythrocyte.  
 FT METAL 58 IRON (HEME DISTAL LIGAND).  
 FT METAL 87 IRON (HEME PROXIMAL LIGAND).  
 SQ SEQUENCE 141 AA; 15303 MW; 8BDCEA7B8DE0DB9 CRC64;  
 Query Match 7.8%; Score 7; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTAL 14  
 |||||  
 Db 105 LVTAL 111

RESULT 8  
 HBA\_ERIEU STANDARD; PRT; 141 AA.  
 ID HBA\_ERIEU  
 AC P01949;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hemoglobin alpha chain.  
 GN HBA.  
 OS Erinnaceus eurypaenus (Western European hedgehog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.  
 OX NCBI\_TaxID=9365;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79109529; PubMed=762046;  
 RA Malta T., Araya A., Matsuda G., Goodman M.;  
 RT "Amino acid sequences of the alpha and beta chains of adult  
 hemoglobin of the European hedgehog, Erinnaceus eurypaenus.";  
 RL J. Biochem. 85:259-268(1979).  
 CC -1- FUNCTION: Involved in oxygen transport from the lung to the  
 CC various peripheral tissues.  
 CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -1- TISSUE SPECIFICITY: Red blood cells.  
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.  
 DR PIR: A02271; HAH.  
 DR HSSP: P01922; IBZ0.  
 DR InterPro: IPR002338; Alpha\_haem.  
 DR InterPro: IPR000971; Globin.  
 DR Pfam: PF00042; globin; 1.  
 DR PRINTS: PR00612; ALPHAAEM.  
 DR PROSITE: PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transport; Erythrocyte.  
 FT METAL 58 IRON (HEME DISTAL LIGAND).  
 FT METAL 87 IRON (HEME PROXIMAL LIGAND).  
 SQ SEQUENCE 141 AA; 15122 MW; E4EE4DE6485050F6 CRC64;  
 Query Match 7.8%; Score 7; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTAL 14  
 |||||  
 Db 105 LVTAL 111

RESULT 9  
 HBA\_RHUN STANDARD; PRT; 141 AA.  
 ID HBA\_RHUN  
 AC P09906;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hemoglobin alpha chain.  
 GN HBA.  
 OS Rhinoceros unicornis (Greater Indian rhinoceros).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Rhinoceros.  
 OX NCBI\_TaxID=9809;

RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=87271129; PubMed=3606819;  
 RA Abdast A., Weber R.E., Braunitzer G., Gollenboch R.;  
 RT "Molecular basis for ATP/2,3-bisphosphoglycerate control switch-over  
 (poikilotherm/homeotherm) an intermediate amino-acid sequence in the  
 RT hemoglobin of the great Indian rhinoceros (Rhinoceros unicornis,  
 RT Perissodactyla).";  
 RL Biol. Chem. Hoppe-Seyler 368:323-332(1987).  
 CC -1- FUNCTION: Involved in oxygen transport from the lung to the  
 CC various peripheral tissues.  
 CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -1- TISSUE SPECIFICITY: Red blood cells.  
 CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY.  
 DR PIR: A26543; A26543.  
 DR HSSP: P01958; IIBE.  
 DR InterPro: IPR002338; Alpha\_haem.  
 DR InterPro: IPR000971; Globin.  
 DR Pfam: PF00042; globin; 1.  
 DR PRINTS: PR00612; ALPHAAEM.  
 DR PROSITE: PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transport; Erythrocyte.  
 FT METAL 58 IRON (HEME DISTAL LIGAND).  
 FT METAL 87 IRON (HEME PROXIMAL LIGAND).  
 SQ SEQUENCE 141 AA; 15319 MW; 9612DA629640B260 CRC64;  
 Query Match 7.8%; Score 7; DB 1; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 7.1;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LVTAL 14  
 |||||  
 Db 105 LVTAL 111

RESULT 10  
 HBA\_TAPTE STANDARD; PRT; 141 AA.  
 ID HBA\_TAPTE  
 AC P01962;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hemoglobin alpha-1 and alpha-2 chains.  
 OS Tapirus terrestris (Lowland tapir) (Brazilian tapir).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.  
 OX NCBI\_TaxID=9801;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85053021; PubMed=6149994;  
 RA Mazur G., Braunitzer G.;  
 RT "Perissodactyla: the primary structure of hemoglobins from the  
 RT lowland tapir (Tapirus terrestris): glutamic acid in position 2 of  
 RT the beta chains.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 365:1057-1106(1984).  
 CC -1- FUNCTION: Involved in oxygen transport from the lung to the  
 CC various peripheral tissues.  
 CC -1- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -1- TISSUE SPECIFICITY: Red blood cells.  
 CC -1- POLYMORPHISM: THERE ARE TWO ALLELES. THE SEQUENCE SHOWN IS THAT OF  
 CC ALPHA-1.  
 DR PIR: A02285; HATPI.  
 DR PIR: A91727; HATP2B.  
 DR HSSP: P01958; 2MB.  
 DR InterPro: IPR002338; Alpha\_haem.  
 DR InterPro: IPR000971; Globin.  
 DR Pfam: PF00042; globin; 1.  
 DR PRINTS: PR00612; ALPHAAEM.  
 DR PROSITE: PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transport; Erythrocyte;  
 KW Polymorphism.  
 FT METAL 58 58 IRON (HEME DISTAL LIGAND).



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RA Smith D.R., Doncette-Stamm L.A., Delonguey C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pochler B., Qiu D.,
RA Spadatoro R., Vitcare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McQuayall S., Shlmer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Neelling J., Reeve J.N.,
RT "Complete genome sequence of Methanobacterium thermotrophicum
RL delta: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7133-7153(1997).
CC -1- SIMILARITY: BELONGS TO THE PCRB FAMILY".
CC -----
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CC -----
DR EMBL: AE000838; AAB85058.1; -.
DR InterPro: IPR003009; FNM enzyme.
DR InterPro: IPR002911; PCRB.
DR Pfam: PF01884; PCRB.1.
DR TIGRFAMs: TIGR00265; PCRB.1.
KW Complete proteome.
SQ SEQUENCE 248 AA; 26525 MW; F59DAE240731E662 CRC64;

Query Match 7.8%; Score 7; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 VKRCTDQ 68
|||||||
Db 191 VKRCTDQ 197

RESULT 15
1A1D_ECOLI STANDARD; PRT; 328 AA.
AC P76316; O08478; O08479;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative L-aminocyclopropane-1-carboxylate deaminase (EC 4.1.99.4)
DE (ACC deaminase).
DE YEDO OR B1919.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
CX NCBI_TaxID=562;
CX [1]
RN RP SEQUENCE FROM N.A.
RN RP STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RL [2]
RN RP SEQUENCE FROM N.A.
RN RP STRAIN=K12;
RX MEDLINE=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasei H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakase S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Tatemoto K., Wada C.,
RA Yamamoto Y., Horikuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map."

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RL DNA Res. 3:379-392(1996).
CC -1- CATALYTIC ACTIVITY: 1-aminocyclopropane-1-carboxylate + H(2)O - 2-
CC Oxobutanoate + NH(3).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACC DEAMINASE FAMILY.
CC -----
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CC -----
CC EMBL; AE000284; AAC74986.1; ALT_INIT.
CC DR EMBL; D90832; BAA15739.1; ALT_INIT.
CC DR EMBL; D90833; BAA15746.1; ALT_INIT.
CC DR EcGene; BG14038; YedO.
CC DR InterPro; IPR001926; B6_enzyme_beta.
CC DR Pfam; PF00291; PALP; 1.
CC DR TIGRFAMs; TIGR01275; ACC_deam_rel; 1.
CC KW Hypothetical protein; Lyase; Pyridoxal phosphate; Complete proteome.
CC FT BINDING 51 51 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SO SEQUENCE 328 AA; 35133 MW; 4179DE645C0B32D8 CRC64;

Query Match 7.8%; Score 7; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AVAAKLG 61
DB 86 AVAAKLG 92

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Search completed: January 2, 2003, 15:00:10  
 Job time : 14 secs



RL Virology 167:485-496(1998).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92196996; PubMed-1549908;  
 RA Handermann M., Schmitzler P., Rosen-Wolff A., Raab K., Sonntag K.C.,  
 RA Darai G.;  
 RT "Identification and mapping of origins of DNA replication within the  
 RT DNA sequences of the genome of insect iridescent virus type 6.";  
 RL Virus Genes 6:19-32(1992).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93118242; PubMed-1475907;  
 RA Sonntag K.C., Darai G.;  
 RT "Characterization of the third origin of DNA replication of the genome  
 RT of insect iridescent virus type 6.";  
 RL Virus Genes 6:333-342(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93260401; PubMed-8492091;  
 RA Stomwasser R., Raab K., Schmitzler P., Janssen W., Darai G.;  
 RT "Identification of the gene encoding the major capsid protein of  
 RT insect iridescent virus type 6 by polymerase chain reaction.";  
 RL J. Gen. Virol. 74:873-879(1993).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94167241; PubMed-8121799;  
 RA Schmitzler P., Hug M., Handermann M., Janssen W., Koonin E.V.,  
 RA Delius H., Darai G.;  
 RT "Identification of genes encoding zinc finger proteins, non-histone  
 RT chromosomal HMG protein homologue, and a putative GTP phosphohydrolase  
 RT in the genome of Chilo iridescent virus.";  
 RL Nucleic Acids Res. 22:158-166(1994).  
 RN [9]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94353641; PubMed-8073636;  
 RA Sonntag K.C., Schmitzler P., Koonin E.V., Darai G.;  
 RT "Chilo iridescent virus encodes a putative helicase belonging to a  
 RT distinct family within the DEAD/H superfamily: Implications for the  
 RT evolution of large DNA viruses.";  
 RL Virus Genes 8:151-158(1994).  
 RN [10]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95213160; PubMed-7698884;  
 RA Sonntag K.C., Schmitzler P., Janssen W., Darai G.;  
 RT "Identification of the primary structure and the coding capacity of  
 RT the genome of insect iridescent virus type 6 between the genome  
 RT coordinates 0.310 and 0.347 (7990 bp).";  
 RL Intervirology 37:287-297(1994).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-94292906; PubMed-8021587;  
 RA Schmitzler P., Sonntag K.C., Muller M., Janssen W., Bugert J.J.,  
 RA Koonin E.V., Darai G.;  
 RT "Insect iridescent virus type 6 encodes a polypeptide related to the  
 RT largest subunit of eukaryotic RNA polymerase II.";  
 RL J. Gen. Virol. 75:1557-1567(1994).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-98141693; PubMed-9482589;  
 RA Bahr U., Tidona C.A., Darai G.;  
 RT "The DNA sequence of Chilo iridescent virus between the genome  
 RT coordinates 0.101 and 0.391: similarities in coding strategy between  
 RT insect and vertebrate Iridoviruses.";  
 RL Virus Genes 15:235-245(1997).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99125223; PubMed-9926400;  
 RA Muller K., Tidona C.A., Bahr U., Darai G.;  
 RT "Identification of a thymidylate synthase gene within the genome of  
 RT Chilo iridescent virus.";  
 RL Virus Genes 17:243-258(1998).  
 RN [14]  
 RP SEQUENCE FROM N.A.

RX MEDLINE-99383793; PubMed-10456793;  
 RA Muller K., Tidona C.A., Darai G.;  
 RT "Identification of a gene cluster within the genome of Chilo  
 RT iridescent virus encoding enzymes involved in viral DNA replication  
 RT and processing.";  
 RL Virus Genes 18:243-264(1999).  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21342589; PubMed-11448171;  
 RA Jakob N.J., Muller K., Bahr U., Darai G.;  
 RT "Analysis of the First Complete DNA Sequence of an Invertebrate  
 RT Iridovirus: Coding Strategy of the Genome of Chilo Irdescent Virus.";  
 RL Virology 286:182-196(2001).  
 RN [16]  
 RP SEQUENCE FROM N.A.  
 RA Jakob N.J., Muller K., Bahr U., Darai G.;  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF303741; AAK82213.1;  
 SQ SEQUENCE 70 AA; 8112 MW; 0098F56C3EB39A42 CRC64;  
  
 Query Match 8.9%; Score 8; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 80 VLVKILKK 87  
 DB 58 VLVKILKK 65  
  
 RESULT 2  
 ID Q9GK65 PRELIMINARY; PRT; 90 AA.  
 AC Q9GK65;  
 DT 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 15, Last sequence update)  
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)  
 DE Lipophilin BL.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LACRIMAL GLAND;  
 RA Zhao C., Nguyen T.X., Lehrer R.I.;  
 RT "Rabbit Lipophilins.";  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF308616; AAG42804.1;  
 DR InterPro: IPR000329; Uteroglobin.  
 DR Pfam: PF01099; Uteroglobin; 1.  
 DR PRINTS: PR00486; UTEROGLBIN.  
 SQ SEQUENCE 90 AA; 9943 MW; 410900DF7F3EB1BC CRC64;  
  
 Query Match 8.9%; Score 8; DB 6; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 10 VTLALCCY 17  
 DB 10 VTLALCCY 17  
  
 RESULT 3  
 ID Q37435 PRELIMINARY; PRT; 217 AA.  
 AC Q37435;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Cytochrome oxidase subunit II.  
 OS Cepaea nemoralis (banded wood snail).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;



OC Helicaceae; Helicidae; Cepaea.  
 OX NCBI\_TaxID=28835;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEPATOPANCREAS;  
 RX MEDLINE=97077301; PubMed=8919868;  
 RA Terrett J.A., Miles S., Thomas R.H.;  
 RT "Complete DNA sequence of the mitochondrial genome of *Cepaea nemoralis*  
 (Gastropoda: Pulmonata).";  
 RL J. Mol. Evol. 42:160-168(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEPATOPANCREAS;  
 RX MEDLINE=97207848; PubMed=9055084;  
 RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,  
 RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,  
 RA Watanabe K., Thomas R.H.;  
 RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons  
 of complete gene organizations of Euhadra, Cepaea and Albinaria and  
 RT implications of unusual tRNA secondary structures.";  
 RL Genetics 145:749-758(1997).  
 DR EMBL: U23045; AAC09520.1; -;  
 DR InterPro: IPR001505; Copper\_CuA.  
 DR InterPro: IPR002429; Cyt\_c-ox\_2.  
 DR InterPro: IPR002088; PPTA.  
 DR InterPro: IPR000822; Znf\_C2H2.  
 DR Pfam: PF00116; COX2; 1.  
 DR Pfam: PF02790; COX2\_TM; 1.  
 DR ProDom: PD000131; Copper\_CuA; 1.  
 DR PROSITE: PS00904; PPTA; UNKNOWN\_1.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; UNKNOWN\_1.  
 KW Mitochondrion.  
 SQ SEQUENCE 217 AA; 25135 MW; 98DAA7B7E0E3DC14 CRC64;  
 Query Match 8.9%; Score 8; DB 8; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 4.1;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LLLVLTAL 14  
 DB 71 LLLVLTAL 78  
 RESULT 4  
 O920J8 PRELIMINARY; PRT; 255 AA.  
 AC O920J8;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Putative outer membrane protein.  
 GN R01322 OR SMC01342.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 OX NCBI\_TaxID=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boissard P., Becker A., Boutry M., Cadieu E., Dreaud S., Gloux S.,  
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
 RA Pohl T., Portetelle D., Puhler A., Purnelle B., Ransperger U.,  
 RA Renard C., Thebaud P., Vandenberg M., Weidner S., Galibert F.;  
 RT Analysis of the chromosome sequence of the legume symbiont  
 RT Sinorhizobium meliloti strain 1021.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL: AL591786; CAC45901.1; -;  
 DR InterPro: IPR000063; Thiorod.  
 DR PROSITE: PS00194; THIOREDOXIN; UNKNOWN\_1.  
 KW Complete proteome.  
 SQ SEQUENCE 255 AA; 27353 MW; 302E0EA668861EE1 CRC64;

Query Match 8.9%; Score 8; DB 16; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 4.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 55 AVAAKLGV 62  
 DB 181 AVAAKLGV 188  
 RESULT 5  
 O65330 PRELIMINARY; PRT; 335 AA.  
 AC O65330;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Acidic chitinase (EC 3.2.1.14).  
 OS Eleagnus umbellata (Autumn olive).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.  
 OX NCBI\_TaxID=43233;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ROOT NODULE;  
 RA Kim H.-B., An C.-S.;  
 RT "Isolation and characterization of cDNA clone encoding acidic  
 RT chitinase from the root nodule of *Eleagnus umbellata*.";  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF061805; AAC16010.1; -;  
 DR HSP: P23951; 2BA.  
 DR InterPro: IPR001002; Chitin\_binding\_1.  
 DR InterPro: IPR00726; Glyco\_hydro\_19.  
 DR Pfam: PF00187; Chitin\_bind\_1; 1.  
 DR Pfam: PF00182; Glyco\_hydro\_19; 1.  
 DR PRINTS: PR00451; CHITINBINDNG.  
 DR ProDom: PD000574; Glyco\_hydro\_19; 1.  
 DR SMART: SM00270; ChnBD; 1.  
 DR PROSITE: PS00773; CHITINASE\_19\_1; 1.  
 DR PROSITE: PS00774; CHITINASE\_19\_2; 1.  
 DR PROSITE: PS00026; CHITIN\_BINDING; 1.  
 KW Chitin binding; Glycosidase; Hydrolase.  
 SQ SEQUENCE 335 AA; 35737 MW; ICC09BB877A18E0 CRC64;  
 Query Match 8.9%; Score 8; DB 10; Length 335;  
 Best Local Similarity 100.0%; Pred. No. 3.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 VCLLVLT 12  
 DB 9 VCLLVLT 16  
 RESULT 6  
 O9HYU9 PRELIMINARY; PRT; 686 AA.  
 AC O9HYU9;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE Hypothetical protein PA3294.  
 GN PA3294.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Muzoguchi S.D., Warrenner P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle V.O., Kowalik D.J., Lagrou M.,

RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lam R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of *Pseudomonas aeruginosa* PAO1, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL: AE004751; AAC06682.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 688 AA; 77042 MW; 844ED9E9BA6D64 CRC64;

Query Match 8.9%; Score 8; DB 16; Length 688;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 APPEAVAA 58  
 |||||||  
 DB 655 APPEAVAA 662

## RESULT 7

O9GK67 PRELIMINARY; PRT; 90 AA.  
 AC O9GK67: 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Lipophilin AL.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LACRIMAL GLAND;  
 RA Zhao C., Nguyen T.X., Lehrer R.I.;  
 RT "Rabbit Lipophilins.";  
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF308614; AAG42802.1; -;  
 DR InterPro: IPR000329; Uteroglobulin.  
 DR Pfam: PF01099; Uterogloblin; 1.  
 DR SMART: SM00096; UTG; 1.  
 SQ SEQUENCE 90 AA; 9762 MW; 6D34F9540C1FF742 CRC64;

Query Match 7.8%; Score 7; DB 6; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 50 DAPPEAV 56  
 |||||||  
 DB 50 DAPPEAV 56

## RESULT 8

O8WMS2 PRELIMINARY; PRT; 96 AA.  
 AC O8WMS2: 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Lipophilin AL2.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LACRIMAL GLAND;  
 RA Lind-Ayres M.R., Crow J.M., Steelman C.A., Nelson J.D.,  
 RA Remington S.G.;  
 RT "Lipophilin AL2 of the male rabbit lacrimal gland.";  
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AY063770; AAL40859.1; -;

DR InterPro: IPR000329; Uterogloblin.  
 DR Pfam: PF01099; Uterogloblin; 1.  
 SQ SEQUENCE 96 AA; 10510 MW; 48EC2972D0EA78C4 CRC64;

Query Match 7.8%; Score 7; DB 6; Length 96;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 TLALCCY 17  
 |||||||  
 DB 11 TLALCCY 17

## RESULT 9

O9BH17 PRELIMINARY; PRT; 102 AA.  
 AC O9BH17: 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE FMRamide-related peptide 2 (Fragment).  
 GN FLP-2.  
 OS Globodera pallida.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.  
 OX NCBI\_TaxID=36090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PA 2/3;  
 RX MEDLINE=21414099; PubMed=11522352.  
 RA Kimber M.J., Fleming C.C., Bjourson A.J., Halton D.W., Maule A.G.;  
 RT "FMRamide-related peptides in potato cyst nematodes.";  
 RL MOL. Biochem. Parasitol. 116:199-208(2001).  
 DR EMBL: AJ300488; CAC32452.1; -;  
 FT CHAIN 89 >98 FMRAMIDE-RELATED PEPTIDE 2.  
 FT NON\_TER 102 102  
 SQ SEQUENCE 102 AA; 11609 MW; A0EB68EB0891A484 CRC64;

Query Match 7.8%; Score 7; DB 5; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 LLLVTLA 13  
 |||||||  
 DB 9 LLLVTLA 15

## RESULT 10

O95Q19 PRELIMINARY; PRT; 107 AA.  
 AC O95Q19: 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Y51H4A.26 protein.  
 GN Y51H4A.26  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sulston J.E.;  
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode *C. elegans*: A platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).  
 DR EMBL: AL132952; CAC70119.1; -;  
 SQ SEQUENCE 107 AA; 12323 MW; 766B3FC05D9C14E0 CRC64;

Query Match 7.8%; Score 7; DB 5; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLVTLA 13  
 |||||  
 Db 7 LLVTLA 13

## RESULT 11

Q91XL7 PRELIMINARY; PRT; 111 AA.  
 AC Q91XL7;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Pancreatic colipase.  
 OS *Spermophilus tridecemlineatus* (Thirteen-lined ground squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
 OC Spermophilus.  
 OX NCBI\_TaxID=43179;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PANCREAS;  
 RT Squire T.L., Bauer V.W., Lowe M.E., Andrews M.T.;  
 RT "Genomic Organization of the Pancreatic Triacylglycerol Lipase Gene in a Hibernating Mammal.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF395869; AAK72258.1; -  
 DR InterPro: IPR001981; Colipase.  
 DR Pfam: PF01114; Colipase; 1.  
 DR Pfam: PF02740; Colipase; 1.  
 DR PROSITE: PS00121; COLIPASE; UNKNOWN.1.  
 SQ SEQUENCE 111 AA; 12056 MW; 1C01F67B2F1ADAB CRC64;

Query Match 7.8%; Score 7; DB 11; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LLVTLA 13  
 |||||  
 Db 6 LLVTLA 12

## RESULT 12

P91445 PRELIMINARY; PRT; 123 AA.  
 AC P91445;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE Hypothetical 14.4 kDa protein.  
 GN t16A1.5.  
 OS *Caenorhabditis elegans*.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; *Caenorhabditis*.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode *C. elegans*: a platform for investigating biology. The *C. elegans* Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Du Z., Goela D.;  
 RT "The sequence of *C. elegans* cosmid t16A1.";  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

## RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U80454; AAB37873.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 123 AA; 14402 MW; D9E9DB1374;C4DP2 CRC64;

Query Match 7.8%; Score 7; DB 5; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KLGKRC 65  
 |||||  
 Db 27 KLGKRC 33

## RESULT 13

O9EX03 PRELIMINARY; PRT; 132 AA.  
 AC O9EX03;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE Hypothetical protein SC01123.  
 GN SC01123 OR ZSCG38.16.  
 OS *Streptomyces coelicolor*.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycinae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra S., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorek A., Woodward J., Barrall B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete *Streptomyces coelicolor* A3(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL445503; CAC13075.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 132 AA; 14688 MW; 08522DBD64286C3C CRC64;

Query Match 7.8%; Score 7; DB 16; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 VAAKGV 62  
 |||||  
 Db 65 VAAKGV 71

## RESULT 14

O985Y1 PRELIMINARY; PRT; 133 AA.  
 AC O985Y1;  
 DT 01-OCT-2001 (TReMBLrel. 18, Created)  
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Hypothetical protein ml17476.  
 GN ML17476.  
 OS *Rhizobium loti* (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-MAEF303099;  
 RX MEDLINE-21082930; PubMed-11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Matsumoto A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 RT Mesorhizobium loti.";  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL; AP003011; BAB3572.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 133 AA; 14765 MW; 7E8FD06159E231A CRC64;

Query Match 7.8%; Score 7; DB 16; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 APPEAVA 57  
 DB 99 APPEAVA 105

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 O82TL9 PRELIMINARY; PRT; 139 AA.  
 AC O82TL9;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Possible heat shock protein, hspX homolog part 1, authentic  
 DE frameshift.  
 DE  
 GN PAE3193A.  
 OS Pyrobaculum aerophilum.  
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
 OC Thermoproteaceae; Pyrobaculum.  
 OX NCBI\_TaxID-13773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IM2 / ATCC 51768 / DSM 7523;  
 RX PubMed-11792869;  
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
 RA Miller J.H.;  
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
 RT aerophilum.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
 DR EMBL; AE009916; AAL64741.1; -;  
 KW Heat shock; Complete proteome.  
 SQ SEQUENCE 139 AA; 14562 MW; 96BE53856A3BE60F CRC64;

Query Match 7.8%; Score 7; DB 17; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 AVAAKLG 61  
 DB 77 AVAAKLG 83

Search completed: January 2, 2003, 15:00:46  
 Job time : 31 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 2, 2003, 14:53:27 : Search time 14 Seconds  
(without alignments)  
189.147 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450  
Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLVKKCSV 90

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	450	100.0	90	3	US-08-821-451A-4
2	450	100.0	90	4	US-09-263-810-4
3	450	100.0	90	4	US-08-912-276-15
4	450	100.0	90	4	US-09-583-169-4
5	450	100.0	90	4	US-09-215-818-6
6	342	76.0	69	4	US-08-821-276-23
7	277	61.6	90	3	US-08-821-451A-2
8	277	61.6	90	4	US-09-263-810-2
9	277	61.6	90	4	US-09-583-169-2
10	219	48.7	90	4	US-08-912-276-22
11	202	44.9	90	3	US-08-821-451A-25
12	202	44.9	90	3	US-08-821-451A-26
13	202	44.9	90	4	US-09-263-810-25
14	202	44.9	90	4	US-09-263-810-26
15	202	44.9	90	4	US-09-583-169-25
16	202	44.9	90	4	US-09-583-169-26
17	110	24.4	91	1	US-08-455-896-8
18	110	24.4	91	2	US-08-933-149-8
19	110	24.4	91	2	US-09-082-343-8
20	110	24.4	91	3	US-09-082-343-8
21	110	24.4	91	5	PCT-US96-08235-8
22	101	22.4	22	4	US-08-912-276-21
23	80	17.8	15	4	US-08-912-276-16
24	75.5	16.7	15	2	US-08-864-725-14
25	75	16.7	15	4	US-08-912-276-19
26	73	16.2	16	4	US-08-912-276-18
27	72	16.0	16	4	US-08-912-276-17

28	70	15.6	109	1	US-07-662-193-5	Sequence 5, App11
29	70	15.6	109	3	US-08-300-928C-8	Sequence 8, App11
30	70	15.6	109	3	US-08-430-944F-8	Sequence 8, App11
31	70	15.6	109	3	US-08-430-014-8	Sequence 8, App11
32	70	15.6	109	3	US-08-431-184-8	Sequence 8, App11
33	69	15.3	1621	4	US-08-972-927-3	Sequence 3, App11
34	66.5	14.8	224	4	US-08-287-959-6	Sequence 6, App11
35	66.5	14.8	3079	5	PCT-US94-0019F-4	Sequence 6, App11
36	66	14.7	16	4	US-08-912-276-20	Sequence 20, App1
37	62	13.8	109	1	US-07-807-529F-6	Sequence 6, App11
38	62	13.8	109	5	PCT-US93-0246F-6	Sequence 6, App11
39	62	13.8	111	1	US-07-662-193-4	Sequence 4, App11
40	62	13.8	111	3	US-08-300-928C-6	Sequence 6, App11
41	62	13.8	111	3	US-08-430-944F-6	Sequence 6, App11
42	62	13.8	111	3	US-08-430-014-6	Sequence 6, App11
43	62	13.8	111	3	US-08-431-184-6	Sequence 6, App11
44	62	13.8	145	2	US-08-832-535-2	Sequence 2, App11
45	62	13.8	145	3	US-09-019-485-2	Sequence 2, App11

#### ALIGNMENTS

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RESULT 1
US-08-821-451A-4
: Sequence 4, Application US/08821451A
: Patent No. 6066724
:
: GENERAL INFORMATION:
: APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz
: TITLE OF INVENTION: Human Endometrial Specific Steroid-
: TITLE OF INVENTION: Binding Factor I, II and III
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
: ADDRESSEE: CECCHI, STEWART & OLSTEIN
: STREET: 6 BECKER FARM ROAD
: CITY: ROSELAND
: STATE: NEW JERSEY
: COUNTRY: USA
: ZIP: 07068
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 INCH DISKETTE
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: WORD PERFECT 5.1
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/821,451A
: FILING DATE: March 21, 1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/014,724
: FILING DATE: March 21, 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: MULLINS, J.G.
: REGISTRATION NUMBER: 33,073
: REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
:
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 90 AMINO ACIDS
: TYPE: AMINO ACID
: STRANDEDNESS:
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PROTEIN
:
: US-08-821-451A-4
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: Query Match 100.0%; Score 450, DB 3; Length 90;
: Best Local Similarity 100.0%; Pred. No. 3.3e+49;
: Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MKLSVCLLVLTALCCYQANAECFALVSELDDFFISPLFKLSLAKFDAPPEAVAAKL 60  
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 Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

# RESULT 2 US-09-263-810-4

; Sequence 4, Application US/09263810  
 ; Patent No. 6174992  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
 ; TITLE OF INVENTION: Human Endometrial Specific Steroid-  
 ; TITLE OF INVENTION: Binding Factor I, II and III  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 ; STREET: 6 BECKER FARM ROAD  
 ; CITY: ROSELAND  
 ; STATE: NEW JERSEY  
 ; COUNTRY: USA  
 ; ZIP: 07068  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 INCH DISKETTE  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WORD PERFECT 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/263,810  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/821,451  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MULLINS, J.G.  
 ; REGISTRATION NUMBER: 33,073  
 ; REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-994-1700  
 ; TELEFAX: 201-994-1744  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 90 AMINO ACIDS  
 ; TYPE: AMINO ACID  
 ; STRANDEDNESS:  
 ; TOPOLOGY: LINEAR  
 ; MOLECULE TYPE: PROTEIN  
 ; US-09-263-810-4

Query Match 100.0%; Score 450; DB 4; Length 90;  
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 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MKLSVCLLVLTALCCYQANAECFALVSELDDFFISPLFKLSLAKFDAPPEAVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

# RESULT 3 US-08-912-276-15

; Sequence 15, Application US/08912276  
 ; Patent No. 6183952  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Billing-Medel, Patricia A.  
 ; APPLICANT: Cohen, Maurice

; APPLICANT: Colpitts, Tracey L.  
 ; APPLICANT: Friedman, Paula N.  
 ; APPLICANT: Gordon, Julian  
 ; APPLICANT: Granados, Edward N.  
 ; APPLICANT: Hodges, Steven C.  
 ; APPLICANT: Klass, Michael R.  
 ; APPLICANT: Kratochvill, Jon D.  
 ; APPLICANT: Roberts-Rapp, Lisa  
 ; APPLICANT: Russell, John C.  
 ; APPLICANT: Stroupe, Steven D.  
 ; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 ; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE BREAST  
 ; NUMBER OF SEQUENCES: 25  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: 100 Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/912,276  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Becker, Cheryl L.  
 ; REGISTRATION NUMBER: 35,441  
 ; REFERENCE/DOCKET NUMBER: 5972.US.P1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 847/935-1729  
 ; TELEFAX: 847/938-2623  
 ; TEXES:  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 90 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: No. 6183952e  
 ; US-08-912-276-15

Query Match 100.0%; Score 450; DB 4; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-49;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

# RESULT 4 US-09-583-169-4

; Sequence 4, Application US/09583169  
 ; Patent No. 6338948  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
 ; TITLE OF INVENTION: Human Endometrial Specific Steroid-  
 ; TITLE OF INVENTION: Binding Factor I, II and III  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

```

ADDRESS: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/583,169
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,451
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-09-583-169-4

Query Match          100.0%; Score 450; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GVKRCTDQMSIQKRSLLAEVLVYKILKCSV 90
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DB 61 GVKRCTDQMSIQKRSLLAEVLVYKILKCSV 90
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RESULT 5
US-09-215-818-6
; Sequence 6, Application US/09215818A
; Patent No. 6379671
; GENERAL INFORMATION:
; APPLICANT: Colpitts, Tracey
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR
; FILE REFERENCE: 5972.US.P2
; CURRENT APPLICATION NUMBER: US/09/215,818A
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/912,276
; EARLIER FILING DATE: 1997-08-17
; EARLIER APPLICATION NUMBER: 08/697,105
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: 08/912,149
; EARLIER FILING DATE: 1997-08-15
; EARLIER APPLICATION NUMBER: 08/697,106
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-215-818-6
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Query Match          100.0%; Score 450; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFFISEPLFKLSLAKFPDAPPAVAKL 60
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QY 61 GVKRCTDQMSIQKRSLLAEVLVYKILKCSV 90
    |||||||
DB 61 GVKRCTDQMSIQKRSLLAEVLVYKILKCSV 90
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RESULT 6
US-08-912-276-23
; Sequence 23, Application US/08912276
; Patent No. 6183952
; GENERAL INFORMATION:
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kralovich, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Stroupe, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE BREAST
; CORRESPONDENCE ADDRESS:
; ADDRESS: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/912,276
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5972.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; INFO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: NO. 6183952e
US-08-912-276-23

Query Match          76.0%; Score 342; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 8e-36;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	82	VKILKRCV 90	
Db	61	VKILKRCV 69	

RESULT 7  
US-08-82

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1 Sequence 2, Application US/08821451A
2 Patent No. 6065724
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4 GENERAL INFORMATION:
5 APPLICANT: Jian NI, Guo-Liang Yu and Retner Gentz
6 TITLE OF INVENTION: Human Endometrial Specific Steroid
7 TITLE OF INVENTION: Blinding Factor I, II and III
8 NUMBER OF SEQUENCES: 27
9
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: CAPELLA, BYRNE, BAIN, GILFILLAN,
12 ADDRESSEE: CECCHI, STEWART & OLSTEIN
13 STREET: 6 BECKER FARM ROAD
14 CITY: ROSELAND
15 STATE: NEW JERSEY
16 COUNTRY: USA
17 ZIP: 07068
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: 3.5 INCH DISKETTE
21
22 COMPUTER: IBM PS/2
23 OPERATING SYSTEM: MS-DOS
24 SOFTWARE: WORD PERFECT 5.1
25
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: US/08/821,451A
28 FILING DATE: March 21, 1997
29 CLASSIFICATION: 435
30
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 60/014,724
33 FILING DATE: March 21, 1996
34 ATTORNEY/AGENT INFORMATION:
35 NAME: MULLINS, J.G.
36 REGISTRATION NUMBER: 33,073
37 REFERENCE/DOCKET NUMBER: 325800-521 (PR257)
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: 201-994-1700
40 TELEFAX: 201-994-1744
41
42 INFORMATION FOR SEQ ID NO: 2:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 90 AMINO ACIDS
45 TYPE: AMINO ACID
46 STRANDEDNESS:
47 TOPOLOGY: LINEAR
48 MOLECULE TYPE: PROTEIN
49
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Query Match	61.6%	Score 277	DB 3	Length 90
Best Local Similarity	58.9%	Pred. No. 1.5e-27		
Matches 53	Conservative 17	Mismatches 20	Indels 0	Gaps 0

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qy      61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV  90
      || ||||:| :| : :|||:|:| |
Db      61 EVKHCTDQISFKRLSLEKVLVEIVKKGCV  90

```

```

RESULT 8
US-09-263-810-2
; Sequence 2, Application US/09263810
; Patent No. 6174992
; GENERAL INFORMATION:

```

1 APPLICANT: JIAN N.I., GUO-LIANG YU AND REINER GENETZ  
 2 TITLE OF INVENTION: Human Endometrial Specific Steroid-  
 3 TITLE OF INVENTION: Binding Factor I, II and III  
 4 NUMBER OF SEQUENCES: 27  
 5 CORRESPONDENCE ADDRESS:  
 6 ADDRESSEE: CARRELLA, BYRNE, BAIN, GILFILLAN,  
 7 ADDRESSEE: CECCHI, STEWART & OLSTEIN  
 8 STREET: 6 BECKER FARM ROAD  
 9 CITY: ROSELAND  
 10 STATE: NEW JERSEY  
 11 COUNTRY: USA  
 12 ZIP: 07068  
 13 COMPUTER READABLE FORM:  
 14 MEDIUM TYPE: 3.5 INCH DISKETTE  
 15 COMPUTER: IBM PS/2  
 16 OPERATING SYSTEM: MS-DOS  
 17 SOFTWARE: WORD PERFECT 5.1  
 18 CURRENT APPLICATION DATA:  
 19 APPLICATION NUMBER: US/09/263,810  
 20 FILING DATE:  
 21 CLASSIFICATION:  
 22 PRIOR APPLICATION DATA:  
 23 APPLICATION NUMBER: 08/821,451  
 24 FILING DATE:  
 25 ATTORNEY/AGENT INFORMATION:  
 26 NAME: MULLINS, J.G.  
 27 REGISTRATION NUMBER: 33,073  
 28 REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
 29 TELECOMMUNICATION INFORMATION:  
 30 TELEPHONE: 201-994-1700  
 31 TELEFAX: 201-994-1744  
 32 INFORMATION FOR SEQ ID NO: 2:  
 33 SEQUENCE CHARACTERISTICS:  
 34 LENGTH: 90 AMINO ACIDS  
 35 TYPE: AMINO ACID  
 36 STRANDEDNESS:  
 37 TOPOLOGY: LINEAR  
 38 MOLECULE TYPE: PROTEIN  
 39 US-09-263-810-2

Query Match	61.68;	Score 277;	DB 4;	Length 90;
Best Local Similarity	58.98;	Pred. No. 1.5e-27;		
Matches	53;	Conservative 17;	Mismatches 20;	Indels 0;
			Gaps	0;

```
QY      61 GVKRCTDQMSLOKRSLIAEVLVLIKCSV  90
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EVKHCTDQISFKRRLSLEKVLVEIVKCGV  90
```

RESULT 9  
US-09-583-169-2  
Sequence 2, Application US/09563169  
Patent No. 6338948  
GENERAL INFORMATION:  
APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid  
TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
Zip: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2



```

1 OPERATING SYSTEM: MS-DOS
2 SOFTWARE: WORD PERFECT 5.1
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/09/583,169
5 FILING DATE:
6 CLASSIFICATION:
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 08/821,451
9 FILING DATE:
10 ATTORNEY/AGENT INFORMATION:
11 NAME: MULLINS, J.G.
12 REGISTRATION NUMBER: 33,073
13 REFERENCE/DOCKET NUMBER: 335800-521 (PF257)
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 201-994-1700
16 TELEFAX: 201-994-1744
17 INFORMATION FOR SEQ ID NO: 2:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 90 AMINO ACIDS
20 TYPE: AMINO ACID
21 STRANDEDNESS:
22 TOPOLOGY: LINEAR
23 MOLECULE TYPE: PROTEIN
24 ;
25 US-09-583-169-2

```

Query Match	61.6%	Score 277	DB 4	Length 90
Best Local Similarity	58.9%	Pred. No. 1.5e-27		
Matches 53	Conservative 17	Mismatches 20	Indels 0	Gaps 0

[illegible]

RESULT 10  
US-08-912-276-22  
; Sequence 22, Application US/08912276

1 APPLICANT: Billing-Medel, Patricia A.  
 2 APPLICANT: Cohen, Maurice  
 3 APPLICANT: Colpitts, Tracey L.  
 4 APPLICANT: Friedman, Paula N.  
 5 APPLICANT: Gordon, Julian  
 6 APPLICANT: Granados, Edward N.  
 7 APPLICANT: Hodges, Steven C.  
 8 APPLICANT: Klass, Michael R.  
 9 APPLICANT: Kratochvill, Jon D.  
 10 APPLICANT: Roberts-Rapp, Lisa  
 11 APPLICANT: Russell, John C.  
 12 APPLICANT: Stroupe, Steven D.  
 13 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 14 FOR DETECTING DISEASES OF THE BREAST  
 15 NUMBER OF SEQUENCES: 25  
 16 CORRESPONDENCE ADDRESS:

1 ADDRESSSEE: Abbott Laboratories  
2 STREET: 100 Abbott Park Road  
3 CITY: Abbott Park  
4 STATE: IL  
5 COUNTRY: USA  
6 ZIP: 60064-3500  
7  
8 COMPUTER READABLE FORM:  
9 MEDIUM TYPE: Diskette  
10 COMPUTER: IBM Compatible  
11 OPERATING SYSTEM: DOS  
12 SOFTWARE: FASTEO for Windows Version 2.0  
13  
14 CURRENT APPLICATION DATA:  
15 APPLICATION NUMBER: US/08/912,276  
16  
17 FILING DATE:

```

1 CLASSIFICATION:
2
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER:
5 FILING DATE:
6 ATTORNEY/AGENT INFORMATION:
7 NAME: Becker, Cheryl L
8 REGISTRATION NUMBER: 35,441
9 REFERENCE/DOCKET NUMBER: 5972. US. P1
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: 847/935-1729
12 TELEFAX: 847/938-2623
13
14 TELEX:
15
16 INFORMATION FOR SEQ ID NO: 22:
17
18 SEQUENCE CHARACTERISTICS:
19
20 LENGTH: 45 amino acids
21 TYPE: amino acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24
25 MOLECULE TYPE: No. 6183952e
26
27 US-08-912-276-22
28
29 Query Match 48.7%; Score 219; DB 4; Length 45;
30 Best Local Similarity 100.0%; Pred. No. 1.2e-20;
31 Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	46	1AKFDAPPEAVAAKLGVRCTDOMSLQKRSLIAEV	YKILTKKCSY	90
DB	1	1AKFDAPPEAVAAKLGVRCTDOMSLQKRSLIAEV <td>YKILTKKCSY</td> <td>45</td>	YKILTKKCSY	45

RESUMÉ 11  
US-08-821-451A-25  
; Sequence 25, Application US/08821451A  
; Patent No. 6066724  
; GENERAL INFORMATION:  
; APPLICANT: Jian Ni, Guo-Liang Yu and Reinher Gentz

1 TYPE OF INVENTION: BIRTHING FACTORY, ... AND ...  
2  
3 NUMBER OF SEQUENCES: 27  
4  
5 CORRESPONDENCE ADDRESS:  
6  
7 ADDRESSEE: CARBILA, BYRNE, BAIN, GILLILLAN,  
8  
9 ADDRESSEE: CECCHI, STEWART & OLSTEIN  
10  
11 STREET: 6 BECKER FARM ROAD  
12  
13 CITY: ROSELAND  
14  
15 STATE: NEW JERSEY  
16  
17 COUNTRY: USA  
18  
19 ZIP: 07068  
20  
21 COMPUTER READABLE FORM:  
22  
23 MEDIUM TYPE: 3.5 INCH DISKETTE  
24  
25 COMPUTER: IBM PS/2  
26  
27 OPERATING SYSTEM: MS-DOS  
28  
29 SOFTWARE: WORD PERFECT 5.1  
30  
31 CURRENT APPLICATION DATA:  
32  
33 APPLICATION NUMBER: US/89/821,451A  
34  
35 FILING DATE: March 21, 1997  
36  
37 CLASSIFICATION: 435  
38  
39 PRIOR APPLICATION DATA:  
40  
41 APPLICATION NUMBER: 60/014,724  
42  
43 FILING DATE: March 21, 1996

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1  ATTORNEY/AGENT INFORMATION:
2
3  NAME: MULLINS, J.G.
4
5  REGISTRATION NUMBER: 33,073
6
7  REFERENCE/DOCKET NUMBER: 325800-521 (PF257)
8
9  TELECOMMUNICATION INFORMATION:
10
11 TELEPHONE: 201-994-1700
12
13 TELEFAX: 201-994-1744
14
15 INFORMATION FOR SEQ ID NO: 25:
16
17     SEQUENCE CHARACTERISTICS:
18
19         LENGTH: 90 AMINO ACIDS
20
21         TYPE: AMINO ACID
22
23         STRANDEDNESS: SINGLE
24
25         TOPOLOGY: LINEAR
26
27         MOLECULE TYPE: PROTEIN
28
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US-08-821-451A-25

Query Match 44.9%; Score 202; DB 3; Length 90;  
Best Local Similarity 48.4%; Pred. No. 3.6e-18;  
Matches 44; Conservative 15; Mismatches 30; Indels 2; Gaps 2;

OY 1 MKLSVCLLVLTALCCYQANA-EPCPALVSELDFFETSEPLFKSLAKFDAPPEAVAK 59  
Db 1 IELSLCLLIM-LAVCCYEANASQICELVAHETISFLMKSEELKLEMYNAPPAVEAK 59  
OY 60 LGVRCCTDOMSLQKRSILAELVYLKIKCSV 90  
Db 60 LEVKRCVDMNSGDRLVVAETLVYIFLECGV 90

RESULT 12

US-08-821-451A-26  
Sequence 26, Application US/08821451A  
Patent No. 606724

GENERAL INFORMATION:

APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-

TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART &amp; OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/821,451A

FILING DATE: March 21, 1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/014,724

FILING DATE: March 21, 1996

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-08-821-451A-26

Query Match 44.9%; Score 202; DB 3; Length 90;  
Best Local Similarity 48.4%; Pred. No. 3.6e-18;  
Matches 44; Conservative 15; Mismatches 30; Indels 2; Gaps 2;

OY 1 MKLSVCLLVLTALCCYQANA-EPCPALVSELDFFETSEPLFKSLAKFDAPPEAVAK 59  
Db 1 IELSLCLLIM-LAVCCYEANASQICELVAHETISFLMKSEELKLEMYNAPPAVEAK 59

OY 60 LGVRCCTDOMSLQKRSILAELVYLKIKCSV 90  
Db 60 LEVKRCVDMNSGDRLVVAETLVYIFLECGV 90

RESULT 13

US-09-263-810-25  
Sequence 25, Application US/09263810  
Patent No. 6174992

GENERAL INFORMATION:

APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-

TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART &amp; OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/263,810

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/821,451

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.

REGISTRATION NUMBER: 33,073

REFERENCE/DOCKET NUMBER: 325800-521 (PF257)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 90 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

US-09-263-810-25

Query Match 44.9%; Score 202; DB 4; Length 90;  
Best Local Similarity 48.4%; Pred. No. 3.6e-18;  
Matches 44; Conservative 15; Mismatches 30; Indels 2; Gaps 2;

OY 1 MKLSVCLLVLTALCCYQANA-EPCPALVSELDFFETSEPLFKSLAKFDAPPEAVAK 59  
Db 1 IELSLCLLIM-LAVCCYEANASQICELVAHETISFLMKSEELKLEMYNAPPAVEAK 59

OY 60 LGVRCCTDOMSLQKRSILAELVYLKIKCSV 90  
Db 60 LEVKRCVDMNSGDRLVVAETLVYIFLECGV 90

RESULT 14

US-09-263-810-26  
Sequence 26, Application US/09263810  
Patent No. 6174992

GENERAL INFORMATION:

APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-

TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART &amp; OLSTEIN

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

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[illegible]

Query Match 44: Conservative 15; Mismatches 30; Indels 2; Gaps 2;  
Best Local Similarity 44.9%; Score 202; DB 4; Length 90;  
48.4%; Pred. No. 3,6e-18;

Oy 1 MKLSVCLLVTLALCCYANA-EPCPALVSELDFFFISEPLFKSLAKEDAPPAVEAAK 59  
Db 1 IELSLCLILIM-LAVCCYEAMASQICDELVAHETISFLMKSEELKEMLMYNAPPAVEAK 59

Oy 60 LGVKRCTDOMSLOKRSLAEVLVKILKKCSV 90  
Db 60 LEVKRCVDMSNGDRLYVAETLVTIFLECGV 90

RESULT 15  
US-09-583-169-25  
Sequence 25, Application US/09583169  
Patent No. 6338948  
GENERAL INFORMATION:  
APPLICANT: Jian NI, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSER: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/583,169  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/821,451  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:



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OM protein - protein search, using sw model

Run on: January 2, 2003, 15:00:53 : Search time 11 seconds  
(without alignments)  
155.058 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 90

Sequence: 1 MKLSVCLLVLTALCYQAN.....IQKRSIAEVLKIKKCSV 90

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Word size : 0

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	90	US-09-825-301-77	Sequence 77, Appl
2	90	100.0	90	US-09-110-716-29	Sequence 29, Appl
3	90	100.0	90	US-09-934-054-1	Sequence 1, Appl
4	90	100.0	90	US-09-985-911-4	Sequence 4, Appl
5	69	76.7	69	US-09-110-716-37	Sequence 37, Appl
6	50	55.6	50	US-09-864-761-44240	Sequence 44240, A
7	8	8.9	74	US-09-110-716-38	Sequence 38, Appl
8	8	8.9	83	US-09-992-598-260	Sequence 260, App
9	8	8.9	83	US-09-989-293A-260	Sequence 260, App
10	8	8.9	83	US-09-989-735-260	Sequence 260, App
11	8	8.9	83	US-09-990-444-260	Sequence 260, App
12	8	8.9	83	US-09-989-730-260	Sequence 260, App
13	8	8.9	83	US-09-990-436-260	Sequence 260, App
14	8	8.9	83	US-09-991-181-260	Sequence 260, App
15	8	8.9	83	US-09-993-687-260	Sequence 260, App
16	8	8.9	83	US-09-989-722-260	Sequence 260, App
17	8	8.9	83	US-09-989-723-260	Sequence 260, App
18	8	8.9	83	US-09-989-279-260	Sequence 260, App
19	8	8.9	83	US-09-989-727-260	Sequence 260, App

20	8	8.9	83	US-09-989-721-260	Sequence 260, App
21	8	8.9	83	US-09-989-732-260	Sequence 260, App
22	8	8.9	83	US-09-991-073-260	Sequence 260, App
23	8	8.9	83	US-09-990-442-260	Sequence 260, App
24	8	8.9	83	US-09-991-163-260	Sequence 260, App
25	8	8.9	83	US-09-993-604-260	Sequence 260, App
26	8	8.9	83	US-09-990-456-260	Sequence 260, App
27	8	8.9	83	US-09-989-721-260	Sequence 260, App
28	8	8.9	90	US-09-985-911-2	Sequence 2, Appl
29	8	8.9	112	US-09-934-034-8	Sequence 8, Appl
30	8	7.8	90	US-09-110-716-27	Sequence 27, Appl
31	7	7.8	166	US-09-815-242-5162	Sequence 5162, App
32	7	7.8	223	US-10-052-586-210	Sequence 210, App
33	7	7.8	288	US-09-925-297-617	Sequence 617, App
34	7	7.8	352	US-09-912-02C-293	Sequence 293, App
35	7	7.8	570	US-08-825-486-2	Sequence 2, Appl
36	7	7.8	570	US-08-870-434-7	Sequence 7, Appl
37	7	7.8	570	US-09-372-044-2	Sequence 2, Appl
38	7	7.8	648	US-09-923-831-43	Sequence 43, Appl
39	7	7.8	739	US-09-974-298-159	Sequence 159, App
40	7	7.8	762	US-09-925-299-998	Sequence 998, App
41	6	6.7	36	US-10-120-319-18	Sequence 18, Appl
42	6	6.7	36	US-09-733-524-11	Sequence 11, Appl
43	6	6.7	43	US-09-864-761-39434	Sequence 39434, A
44	6	6.7	43	US-09-864-761-41268	Sequence 41268, A
45	6	6.7	45	US-09-864-761-36472	Sequence 36472, A

#### ALIGNMENTS

RESULT 1  
US-09-825-301-77  
; Sequence 77, Application US/09825301  
; Patent No. US20020009738A1  
; GENERAL INFORMATION:  
; APPLICANT: Houghton, Raymond L.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Molesh, David A.  
; APPLICANT: Xu, Jiaqun  
; APPLICANT: Zehentner, Barbara  
; TITLE OF INVENTION: PERSING, David H.  
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION  
; FILE REFERENCE: 210121.513  
; CURRENT APPLICATION NUMBER: US/09/825,301  
; CURRENT FILING DATE: 2001-04-02  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 77  
; LENGTH: 90  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-825-301-77  
  
Query Match 100.0%: Score 90; DB 10; Length 90;  
Best Local Similarity 100.0%: Pred. No. 1.8e-81;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MKLSVCLLVLTALCYQANAEPCPALVSELDFFITSEPLFKSLAKFDAPPAVAATL 60  
DB 61 GYKRCIDQMSLQKRSIAEVLKIKKCSV 90  
DB 61 GYKRCIDQMSLQKRSIAEVLKIKKCSV 90  
  
RESULT 2  
US-09-110-716-29  
; Sequence 29, Application US/09110716A  
; Patent No. US20020034739A1  
; GENERAL INFORMATION:

APPLICANT: Lehrer, Robert I.  
APPLICANT: Zhao, Chengquan  
TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS  
FILE REFERENCE: 22000-20596.00  
CURRENT APPLICATION NUMBER: US/09/110,716A  
CURRENT FILING DATE: 1998-07-07  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 90  
TYPE: PRT  
ORGANISM: lipophilin B  
US-09-110-716-29

Query Match  
Best Local Similarity 100.0%; Score 90; DB 10; Length 90;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90  
DB 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90

RESULT 3  
US-09-934-054-1  
Sequence 1, Application US/09934054  
Patent No. US20020107385A1  
GENERAL INFORMATION:  
APPLICANT: Akerblom, Ingrid E.  
Hillman, Jennifer L.  
Murry, Lynn E.  
Goli, Surya K.  
Hawkins, Phillip R.  
TITLE OF INVENTION: BREAST TUMOR SPECIFIC PROTEINS  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 2200 Sand Hill Road, Suite 100  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025-6936  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/934,054  
FILING DATE: 21-Aug-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/747,547  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0077 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: <Unknown>  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-934-054-1

Query Match  
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90  
DB 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90

RESULT 4  
US-09-985-911-4  
Sequence 4, Application US/09985911  
Patent No. US20020151012A1  
GENERAL INFORMATION:  
APPLICANT: NI ET AL.  
TITLE OF INVENTION: HUMAN ENDOMETRIAL SPECIFIC STEROID-BINDING FACTOR I, II AND II  
FILE REFERENCE: PF257D3  
CURRENT APPLICATION NUMBER: US/09/985,911  
CURRENT FILING DATE: 2001-11-06  
PRIOR APPLICATION NUMBER: 09/583,169  
PRIOR FILING DATE: 2000-05-30  
PRIOR APPLICATION NUMBER: 09/263,810  
PRIOR FILING DATE: 1999-03-08  
PRIOR APPLICATION NUMBER: 08/821,451  
PRIOR FILING DATE: 1997-03-21  
PRIOR APPLICATION NUMBER: 60/014,724  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 90  
TYPE: PRT  
ORGANISM: human  
US-09-985-911-4

Query Match  
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DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAAKL 60

QY 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90  
DB 61 GVKRCTDMSLQKRSLSIAEVLVKILKCSV 90

RESULT 5  
US-09-110-716-37  
Sequence 37, Application US/09110716A  
Patent No. US20020034739A1  
GENERAL INFORMATION:  
APPLICANT: Lehrer, Robert I.  
APPLICANT: Zhao, Chengquan  
TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS  
FILE REFERENCE: 22000-20596.00  
CURRENT APPLICATION NUMBER: US/09/110,716A  
CURRENT FILING DATE: 1998-07-07  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 37  
LENGTH: 69  
TYPE: PRT  
ORGANISM: Lpnb  
US-09-110-716-37

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Query Match          76.7%: Score 69; DB 10; Length 69;
Best Local Similarity 100.0%: Pred. No. 9.9e-61;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 82 VKILKCSV 90
DB 61 VKILKCSV 69

RESULT 6
US-09-864-761-44240
; Sequence 44240, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SEQ ID NO 44240
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004127.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1

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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: AW103293.1, EVALUE 5.00e-21
; OTHER INFORMATION: SWISSPROT HIT: 095969, IVALUE 4.00e-22
US-09-864-761-44240

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Best Local Similarity 100.0%: Pred. No. 2.7e-42;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LDFFIISPLEFKLSLAKFDAPPEAVAAKLGKCTDMSLQKRSLLAEVL 50

RESULT 7
US-09-110-716-38
; Sequence 38, Application US/09110716A
; Patent No. US20020034739A1
; GENERAL INFORMATION:
; APPLICANT: Lehner, Robert I.
; APPLICANT: Zhao, Chengquan
; APPLICANT: Glasgow, Benjamin J.
; TITLE OF INVENTION: PEPTIDES CHARACTERISTIC OF CERTAIN TUMORS
; FILE REFERENCE: 22000-20596.00
; CURRENT FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 74
; TYPE: PRT
; ORGANISM: PRC2
US-09-110-716-38

Query Match          8.9%: Score 8; DB 10; Length 74;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 28 FDAPPEAV 35

RESULT 8
US-09-992-598-260
; Sequence 260, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

```

APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC20  
CURRENT FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
PRIOR FILING DATE: 1998-06-02  
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PRIOR FILING DATE: 1998-06-02  
PRIOR APPLICATION NUMBER: 60/087827  
PRIOR FILING DATE: 1998-06-03  
PRIOR APPLICATION NUMBER: 60/088021  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088025  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088026  
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PRIOR APPLICATION NUMBER: 60/088742  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088824  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088826

PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088861  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/088876  
PRIOR FILING DATE: 1998-06-11  
PRIOR APPLICATION NUMBER: 60/089105  
PRIOR FILING DATE: 1998-06-12  
PRIOR APPLICATION NUMBER: 60/089440  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
PRIOR FILING DATE: 1998-06-16  
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PRIOR FILING DATE: 1998-06-16  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-17  
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PRIOR FILING DATE: 1998-06-18  
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PRIOR FILING DATE: 1998-06-25



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PRIOR FILING DATE: 1998-06-25  
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PRIOR FILING DATE: 1998-06-25  
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PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091626  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 8.9% Score 8: DB 9: Length 83:  
Best Local Similarity 100.0%: Pred.No. 0.48;  
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 12 LALCCYQA 19  
DB 12 LALCCYQA 19

RESULT 9  
US-09-989-293A-260  
Sequence 260, Application US/09889293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Getter, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730PIC66  
CURRENT APPLICATION NUMBER: US/09/989,293A

CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
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PRIOR FILING DATE: 1998-06-11

;; PRIOR APPLICATION NUMBER: 60/089105  
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;; PRIOR APPLICATION NUMBER: 60/091544  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYOA 19  
Db 12 LALCCYOA 19

RESULT 10  
US-09-989-735-260  
;; Sequence 260, Application US/09989735  
;; Publication No. US20020193299A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnovers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Grimaldi, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P1C61  
;; CURRENT APPLICATION NUMBER: US/09/989,735  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/065186  
;; PRIOR FILING DATE: 1997-11-12

[illegible]

PRIOR APPLICATION NUMBER: 60/091478  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LALCCYQA 19  
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DB 12 LALCCYQA 19

RESULT 11  
US-09-990-444-260  
Sequence 260, Application US/09990444  
Publication No. US20020193300A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730P1C19  
CURRENT APPLICATION NUMBER: US/09/990,444  
PRIOR FILING DATE: 2001-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
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PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20  
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PRIOR FILING DATE: 1998-04-28  
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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09  
  
Query Match 8.9%; Score 8; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0 48;  
Matches 8; Conservative 0; Mismatched 0; Indels 0; Gaps 0;  
  
QY 12 LALCYOA 19  
DB 12 LALCYOA 19  
  
RESULT 12  
US-09-989-730-260  
; Sequence 260, Application US/09989730  
; Publication No. US20020197674A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerlitsen, Mary E.  
; APPLICANT: Goddard, Audrey J.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kjaavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC69  
; CURRENT APPLICATION NUMBER: US/09/989,730  
;; PRIOR FILING DATE: 2001-11-20  
;; PRIOR APPLICATION NUMBER: 60/049787  
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;; PRIOR FILING DATE: 1998-05-28

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PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
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Query Match      8.9%; Score 8; DB 9; Length 83;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      12 LALCCYQA 19
Db      12 LALCCYQA 19

RESULT 13
US-09-990-436-260
; Sequence 260, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC14
; CURRENT APPLICATION NUMBER: US/09/990,436
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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Query Match 8.9%; Score 8; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCCYCA 19  
Db 12 LALCCYCA 19

RESULT 14  
US-09-991-181-260  
Sequence 260, Application US/09991181  
Publication No. US20020197615A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bolstein, David  
APPLICANT: Deenoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J Christopher  
APPLICANT: Guiney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumasi, Daniel  
APPLICANT: Watanabe, Collin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC53  
CURRENT FILING DATE: 2001-11-16  
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PRIOR FILING DATE: 1997-06-16  
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Query Match 8.9%; Score 8; LB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LALCCYQA 19  
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Db 12 LALCCYQA 19

RESULT 15  
US-09-993-687-260

Sequence 260, Application US/09993687  
Publication No. US20020198149A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
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APPLICANT: Klavins, Ivar J.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730pic11  
CURRENT FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
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PRIOR APPLICATION NUMBER: 60/088212  
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PRIOR APPLICATION NUMBER: 60/088217  
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PRIOR APPLICATION NUMBER: 60/088655  
PRIOR FILING DATE: 1998-06-09  
PRIOR APPLICATION NUMBER: 60/088734  
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PRIOR FILING DATE: 1998-06-12  
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PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089512  
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PRIOR APPLICATION NUMBER: 60/089514  
PRIOR FILING DATE: 1998-06-16  
PRIOR APPLICATION NUMBER: 60/089532  
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PRIOR APPLICATION NUMBER: 60/089653  
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PRIOR APPLICATION NUMBER: 60/090254  
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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/090540  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090542  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090557  
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;; PRIOR FILING DATE: 1998-06-26  
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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
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;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 8.9%; Score 8; DB 9; Length 83;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 LALCXYQA 19  
| | | | | | | |  
Db 12 LALCXYQA 19

Search completed: January 2, 2003, 15:04:37  
Job time : 12 secs





XX Gentz RL, NI J, Yu G;  
 PI WPI: 1997-480206/44.  
 DR N-PSDB; AAT94831.  
 XX Human endometrial specific steroid-binding factor I, II and III -  
 PT used to treat inflammation, asthma, rhinitis, cystic fibrosis,  
 PT airway disease, neoplasia, atopy etc.  
 PS Claim 18; Page 63-64; 92pp; English.  
 XX This sequence comprises human endometrial specific steroid binding  
 CC factor II (ESF II), a protein that inhibits phospholipase A2  
 CC activity, binds to polychlorinated biphenyl compounds, reduces  
 CC foreign protein antigenicity, inhibits monocyte and neutrophil  
 CC chemotaxis and phagocytosis, inhibits platelet aggregation,  
 CC regulates eicosanoid levels in the human uterus and controls the  
 CC growth of endometrial cells. The amino acid sequence was deduced  
 CC from a cDNA clone (see AAT94831) derived from cycloheximide-treated  
 CC CEM cells. ESF I (see AAW35802) and ESF III (see AAW35804) are also  
 CC claimed. Human ESF II has about 49% identity with rat prostatic  
 CC steroid-binding protein. Recombinant ESF I, II and III can be  
 CC expressed in host cells for use in claimed methods (a) for treating  
 CC a patient in need of ESF I, II or III (including expression of the  
 CC polypeptide in vivo) and (b) for identifying compounds which bind  
 CC to and inhibit activation of the ESF polypeptide. hESF I, II and  
 CC III may be used to treat inflammation, asthma, rhinitis, cystic  
 CC fibrosis, airway disease, neoplasia and atopy.  
 XX Sequence 90 AA:  
 SQ  
 Query Match 100.0%; Score 450; DB 18; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60  
 DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60  
 QY 61 GVKRCTDOMSLQKRSLLAEVLVKILKKCSV 90  
 DB 61 GVKRCTDOMSLQKRSLLAEVLVKILKKCSV 90  
 RESULT 2  
 AAW59776  
 ID AAW59776 standard; Protein: 90 AA.  
 XX AAW59776;  
 AC AAW59776;  
 XX 12-OCT-1998 (first entry)  
 DT 12-OCT-1998 (first entry)  
 XX Amino acid sequence of the human steroid binding protein C1.  
 DE Human steroid-binding protein C1; hSBP1, hSBP2; breast cancer; probe;  
 KW gene therapy vector; ribozyme; probe; hybridisation; amplification;  
 KW antibody; immunoassay.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO9821331-A1.  
 PN WO9821331-A1.  
 XX 22-MAY-1998.  
 PD 22-MAY-1998.  
 XX 07-NOV-1997; 97WO-US20674.  
 PE 07-NOV-1997; 97WO-US20674.  
 XX 12-NOV-1996; 96US-0747547.  
 PR 12-NOV-1996; 96US-0747547.  
 XX (INCY-) INCYTE PHARM INC.  
 PA (INCY-) INCYTE PHARM INC.  
 XX Akerblom IE, Goli SK, Hawkins PR, Hillman JL, Murry LE;  
 PI Akerblom IE, Goli SK, Hawkins PR, Hillman JL, Murry LE;

DR WPI: 1998-297935/26.  
 DR N-PSDB; AAV41579.  
 XX New human steroid binding proteins C1 and C2 - useful for, e.g.  
 PT diagnosis, monitoring and treating breast cancer, and for drug  
 PT screening  
 PS Claim 1; Fig 1; 70pp; English.  
 XX This is the amino acid sequence of the human steroid-binding protein  
 CC C1 (hSBP1) used in the method of the invention for the diagnosis,  
 CC monitoring and treatment of breast cancer. hSBP1 and hSBP2 are useful  
 CC as markers for breast cancer, i.e. measuring levels of hSBP1 and hSBP2  
 CC used for diagnosis or monitoring the disease, to identify subjects  
 CC at risk and to discriminate between different forms of cancer for  
 CC selection of appropriate therapies. They may also be used for drug  
 CC screening. Nucleic acids encoding hSBP1 and hSBP2 can be used in gene  
 CC therapy vectors to overexpress the steroid-binding proteins, preventing  
 CC binding of steroids, or antisense sequences, ribozymes. Their nucleic  
 CC acids can also be used for the diagnosis and monitoring (by quantifying  
 CC expression of hSBP), as source of probes for hybridisation and  
 CC amplification of genomic or related sequences for studying regulation of  
 CC gene function and for mapping the genomic sequence. Antibodies are used  
 CC as diagnostic reagents in standard immunoassays for hSBP.  
 XX Sequence 90 AA:  
 SQ  
 Query Match 100.0%; Score 450; DB 19; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60  
 DB 1 MKLSVCLLVLTALCCYQANAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEVAAKL 60  
 QY 61 GVKRCTDOMSLQKRSLLAEVLVKILKKCSV 90  
 DB 61 GVKRCTDOMSLQKRSLLAEVLVKILKKCSV 90  
 RESULT 3  
 AAW54271  
 ID AAW54271 standard; Protein: 90 AA.  
 XX AAW54271;  
 AC AAW54271;  
 XX 29-JUL-1998 (first entry)  
 DT 29-JUL-1998 (first entry)  
 XX BU101 antigenic peptide epitope 1.  
 DE BU101 antigenic peptide epitope 1.  
 XX BU101; breast cancer; diagnosis; prevention; treatment; gene therapy;  
 KW immunisation; drug screening; epitope.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX WO9807857-A1.  
 PN WO9807857-A1.  
 XX 26-FEB-1998.  
 PD 26-FEB-1998.  
 XX 19-AUG-1997; 97WO-US14665.  
 PE 19-AUG-1997; 97WO-US14665.  
 XX 15-AUG-1997; 97US-0912276.  
 PR 15-AUG-1997; 97US-0912276.  
 XX 19-AUG-1996; 96US-0697105.  
 PR 19-AUG-1996; 96US-0697105.  
 XX (ABBO) ABBOTT LAB.  
 PA (ABBO) ABBOTT LAB.  
 XX Billing-medel PA, Cohen M, Colpitts TL, Friedman PN;  
 PI Gordon J, Granadosen, Hodges SC, Klass MR, Kratochvil JD;  
 PI Roberts-rapp L, Russell JC, Stroupe SD;  
 XX WPI: 1998-169161/15.  
 DR N-PSDB; AAV26461.  
 XX

PT New BU101 protein over-expressed in breast cancer - useful for, e.g.  
 PT diagnosis, treatment and prevention of breast cancer  
 XX  
 PS Claim 17; Page 90; 105pp; English.  
 XX  
 CC This represents a BU101 polypeptide sequence. BU101 is a member of the  
 CC uteroglobin family of proteins and is over-expressed in breast cancer.  
 CC Cells transfected with a recombinant expression system comprising a  
 CC sequence derived from the BU101 open reading frame and with at least 50  
 CC percent identity to the sequences shown in AAY26458 to AAY26461 are used  
 CC to produce BU101 polypeptides containing at least 1 epitope. These are  
 CC used to detect BU101-specific antibodies which are used correspondingly  
 CC to detect BU101 antigens. The BU101 polynucleotide sequences can be used  
 CC in a method for detecting the presence of a target BU101 polynucleotide.  
 CC The various assays are used for diagnosis, prognosis, staging,  
 CC monitoring, treating and preventing diseases of the breast (especially  
 CC cancer and its metastases), and also for determining susceptibility. The  
 CC BU101 polypeptides are also useful in drug screening, e.g. to identify  
 CC antagonists of BU101, potentially useful therapeutically and as targets  
 CC for therapy. The antibodies are also useful for targeted drug delivery  
 CC and therapeutically to neutralise BU101 polypeptides. Fragments of the  
 CC BU101 nucleic acid are useful as probes and primers, e.g. for detection  
 CC of altered gene expression or in fluorescent in situ hybridisation, also  
 CC in gene therapy to generate antisense or ribozyme molecules or for  
 CC genetic immunisation.  
 CC  
 XX  
 SQ Sequence 90 AA;  
 Query Match 100.0%; Score 450; DB 19; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFETSEPLFKSLAKFDAPPVAAKL 60  
 DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFETSEPLFKSLAKFDAPPVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 RESULT 4  
 AAM89613  
 ID AAM89613-standard; Protein; 90 AA.  
 AC AAM89613;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Endometrial steroid binding protein II.  
 XX  
 KW Endometrial steroid binding protein II; ESBPII; cancer; detection;  
 KW endometriosiis; endometrial fibroid; mammary cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN MO9856248-A1.  
 XX  
 PD 17-DEC-1998.  
 XX  
 PF 09-JUN-1998; 98WO-US12053.  
 XX  
 PR 09-JUN-1997; 97US-0049015.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Schmidt CJ, Wang X;  
 XX  
 DR WPI: 1999-080843/07.  
 DR N-PSDB; AAX00069.  
 XX  
 PT Treatment of endometrial cancer, mammary cancer, endometriosiis or  
 PT endometrial fibroids - comprises administering endometrial steroid

PT binding protein II antagonist  
 XX  
 PS Disclosure; Page 13; 19pp; English.  
 XX  
 CC A method has been developed for the treatment of endometrial cancer,  
 CC mammary cancer, endometriosiis or endometrial fibroids. The method  
 CC comprises administering endometrial steroid binding protein II (ESBPII)  
 CC antagonist. Also described in the present invention are: (1) a method  
 CC for diagnosing the above mentioned diseases comprising analysing the  
 CC abnormally high level of ESBPII polypeptide in cells, tissues and bodily  
 CC fluids; and (2) a diagnostic method for the diseases described above  
 CC comprising analysing the abnormally high or low transcription level of  
 CC ESBPII in cells, tissues and bodily fluids. The methods can be used to  
 CC diagnose, treat, and monitor the progression, remission or recurrence of  
 CC abnormal cell growth, such as cancers, especially endometrial and  
 CC mammary cancer, and endometriosiis and endometrial fibroids. The present  
 CC sequence represents ESBPII, from the present invention.  
 CC  
 XX  
 SQ Sequence 90 AA;  
 Query Match 100.0%; Score 450; DB 20; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFETSEPLFKSLAKFDAPPVAAKL 60  
 DB 1 MKLSVCLLVTLALCCYQANAEPCPALVSELDFFETSEPLFKSLAKFDAPPVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 RESULT 5  
 AAB13787  
 ID AAB13787 standard; Protein; 90 AA.  
 AC AAB13787;  
 XX  
 DT 20-JUN-2001 (first entry)  
 XX  
 DE Human BU101.  
 XX  
 KW Human; breast cancer; breast disease detection; mammagloblin;  
 KW uteroglobin; BU101; endometrial; cytosatic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 53 /label=Leu  
 FT /note="Encoded by C76 in polymorphic variant"  
 XX  
 PN WO200035950-A2.  
 XX  
 PD 22-JUN-2000.  
 XX  
 PF 20-DEC-1999; 99WO-US30489.  
 XX  
 PR 18-DEC-1998; 98US-0215818.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Colpitts TL, Russell JE;  
 XX  
 DR WPI: 2000-442366/38.  
 DR N-PSDB; AAA64846.  
 XX  
 PT Multimeric polypeptide antigen and antibody specific to the antigen are  
 PT useful for diagnosing, detecting and treating breast cancer -  
 PS Claim 1; Page 124; 124pp; English.  
 XX

CC BU101 is a member of the uteroglobin protein family. The present  
 CC sequence is the protein sequence for human BU101. The present  
 CC invention relates to a multimeric polypeptide antigen, which comprises  
 CC of the present sequence and mamaglobin polypeptide (AAB13786).  
 CC Mamaglobin is another uteroglobin protein. The presence of multimeric  
 CC polypeptide antigen in a test sample can be used as the basis for a test  
 CC to diagnose breast disease e.g. breast cancer, in a patient. The  
 CC detection can be carried out using antibodies specific for the multimeric  
 CC polypeptide antigen. The present sequence can either have a Pro or Leu  
 CC residue at position 53, since the coding sequence has a single  
 CC nucleotide T/C polymorphism at nucleotide position 254.  
 XX  
 SQ Sequence 90 AA;  
 Query Match 100.0%; Score 450; DB 21; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPFLKLSLAKEDAPPEAVAAKL 60  
 DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPFLKLSLAKEDAPPEAVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSY 90  
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSY 90  
 RESULT 6  
 AAB07501  
 ID AAB07501 standard; Protein; 90 AA.  
 AC AAB07501;  
 XX  
 DT 20-OCT-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human BU101 polypeptide.  
 XX  
 KW Human; BU101; breast disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200041516-A2.  
 XX  
 PD 20-JUL-2000.  
 XX  
 PF 19-JAN-2000; 2000MO-US01309.  
 XX  
 PR 19-JAN-1999; 99US-0233693.  
 XX  
 PA (ABBO ) ABBOTT LAB.  
 XX  
 PI Billing-medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
 PI Granados EN, Hodges SC, Klass MR, Kratochvill JD, Roberts-rapp L;  
 PI Russell JC, Scheffel CP, Stroupe SD;  
 XX  
 DR WPI: 2000-475906/41.  
 DR N-PSDB: AAA58880.  
 XX  
 PT detection presence of target BU101 polynucleotide in sample useful for  
 PT detection of breast cancer, comprises contacting sample with  
 PT BU101-specific polynucleotide and determining binding -  
 XX  
 PS Claim 23; Page 125; 127pp; English.  
 CC  
 CC The present sequence represents a BU101 polypeptide. The BU101 gene is  
 CC transcribed from breast tissue. The specification describes a method for  
 CC detecting the presence of a target BU101 polynucleotide in a test  
 CC sample. The method comprises contacting the sample with at least one  
 CC BU101-specific polynucleotide (AA58875-80), and detecting bound  
 CC polynucleotides. The method and BU101 polynucleotides are useful for  
 CC detecting the presence of BU101 polynucleotides. The methods may be  
 CC used for the diagnosis of breast disease, indicated by the formation  
 CC of complexes.

XX  
 SQ Sequence 90 AA;  
 Query Match 100.0%; Score 450; DB 21; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPFLKLSLAKEDAPPEAVAAKL 60  
 DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFFFISSPFLKLSLAKEDAPPEAVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSY 90  
 DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSY 90  
 RESULT 7  
 AAB03768  
 ID AAB03768 standard; Protein; 90 AA.  
 AC AAB03768;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human endometrial specific steroid-binding factor II protein sequence.  
 XX  
 KW Endometrial specific steroid-binding factor; human; hESF; inflammation;  
 KW asthma; rhinitis; cystic fibrosis; air way disease; neoplasia; atopy;  
 KW eicosanoid level regulator; chemotaxis inhibitor; endometrial cancer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US606724-A.  
 XX  
 PD 23-MAY-2000.  
 XX  
 PF 21-MAR-1997; 97US-0821451.  
 XX  
 PR 21-MAR-1996; 96US-0014724.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Yu G, Gentz R, Ni J;  
 PI  
 DR WPI: 2000-375600/32.  
 DR N-PSDB: AAA59729.  
 XX  
 PT Novel gene encoding human endometrial specific steroid-binding factor  
 PT I, II and III which is useful for treating asthma, rhinitis, cystic  
 PT fibrosis, airway disease and neoplasia -  
 XX  
 PS Claim 1; Fig 2; 36pp; English.  
 CC  
 CC This invention relates to nucleic acid molecules encoding portions of the  
 CC human endometrial specific steroid-binding factors I, II, and III. Also  
 CC included in the invention are hESF I, II, and III polypeptide sequences.  
 CC The nucleotide sequence exhibit antiasthmatic, antiinflammatory,  
 CC antiallergic, and cytoskeletal properties. The polynucleotides are used in  
 CC gene therapy to express hESF I, II and III polypeptides in vivo to treat  
 CC and/or prevent inflammation, asthma, rhinitis, cystic fibrosis, air way  
 CC disease, neoplasia and atopy. The polynucleotides are also used to  
 CC inhibit phospholipase A2 activity, bind polychlorinated biphenyls, reduce  
 CC foreign protein antigenicity, inhibit monocyte and neutrophil chemotaxis  
 CC and phagocytosis, inhibit platelet aggregation, regulate eicosanoid  
 CC levels in the human uterus and control the growth of endometrial cells.  
 CC The polynucleotides are also useful for detecting complementary  
 CC polynucleotides as a diagnostic reagent. The hESF I, II and III  
 CC polynucleotides are used to detect complementary polynucleotides such as  
 CC a diagnostic reagent. Detection of a mutated form of hESF I, II and III  
 CC associated with a dysfunction will provide a diagnostic tool that can  
 CC define diagnosis of a disease or susceptibility to a disease which  
 CC results from under-expression, over-expression or altered expression of  
 CC hESF I, II and III e.g. a susceptibility to inherited asthma and



CC endometrial cancer. They are also useful for chromosome identification.  
CC The present sequence represents a hsf II protein sequence identified in  
CC the invention.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 21; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFEFISBPFLKSLAKFPAPPAVAKL 60  
DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFEFISBPFLKSLAKFPAPPAVAKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 8  
AA84875

ID AA84875 standard; Protein; 90 AA.

XX AC AA84875;

DT 08-AUG-2000 (first entry)

XX A human endometrial specific steroid-binding protein II.

XX Human; endometrial specific steroid-binding protein II; ESHPII;  
KM breast tumour; prostate cancer; gynaecological cancer; cancer;  
XX endometrial cancer; ovarian cancer; uterine cancer.

OS Homo sapiens.

XX WO200020043-A1.

PN 13-APR-2000.

PD 05-OCT-1999; 99WO-US23252.

PR 05-OCT-1998; 98US-0103093.

PA (DIAD-) DIADEXUS LLC.

XX Macina RA;

DR WPI; 2000-303648/26.

DR N-PSDB; AAA14953.

XX Diagnosing, staging, monitoring, imaging and treating prostate and  
PT gynaecological cancers by measuring levels of endometrial specific  
XX steroid-binding protein (ESBP)II expression  
PS Claim 6; Page 31-32; 35pp; English.

XX The present sequence represents a human endometrial specific steroid-  
CC binding protein (ESBP) II. The ESBPII protein is overexpressed in  
CC breast tumours. The specification describes a method for diagnosing  
CC prostate or a gynaecological cancer. The method comprises measuring  
CC levels of ESBPII in cells, tissues or body fluids of a patient, and  
CC comparing this to levels from a normal control, where a variance in  
CC levels indicates cancer. The method is used to diagnose, stage, monitor,  
CC image or treat prostate or gynaecological cancer. The gynaecological  
CC cancers include breast, endometrial, ovarian and uterine cancer.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 21; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFEFISBPFLKSLAKFPAPPAVAKL 60

DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFEFISBPFLKSLAKFPAPPAVAKL 60

OY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
DB 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 9  
AAG65989

ID AAG65989 standard; Protein; 90 AA.

XX AC AAG65989;

DT 11-FEB-2002 (first entry)

XX Lipophilin B polypeptide.

XX Genetic subtraction; DNA microarray analysis; polymerase chain reaction;  
KM cancer; B726P; Lipophilin B; mammaglobin.

XX Homo sapiens.

XX WO200175171-A2.

PD 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10631.

PR 03-APR-2000; 2000US-194241P.

PR 20-JUL-2000; 2000US-219862P.

PR 27-JUL-2000; 2000US-221300P.

PR 18-DEC-2000; 2000US-256592P.

XX (CORI-) CORIXA CORP.

XX Houghton RL, Dillon DC, Molesh DA, Yu J, Zehentner B, Persing DH;

DR WPI; 2001-626449/72.

DR N-PSDB; AA167269.

XX Identifying tissue (tumour)-specific polynucleotides overexpressed in  
PT tissue of interest as compared to control tissue, for detecting cancer  
PT cells in patient, comprises DNA microarray analysis or quantitative  
PT polymerase chain reaction -  
XX Examples; Page 127; 127pp; English.

XX The invention relates to identifying tissue-specific polynucleotides (P)  
CC that involves performing a genetic subtraction to identify pool of (P)  
CC from tissue of interest (TI), performing DNA microarray analysis to  
CC identify first subset of polynucleotides (SP1) at least 2-fold over  
CC expressed in TI, and performing quantitative polymerase chain reaction  
CC (PCR) analysis on SP1 to identify second subset of (P). The method is  
CC useful for determining the presence or absence of a cancer cell in a  
CC patient, monitoring the progression of cancer in a patient using a  
CC biological sample such as blood, serum, lymph nodes, bone marrow, sputum,  
CC urine or a tumour biopsy sample. The methods are useful for determining  
CC the presence or absence of or monitoring progression of prostate, breast,  
CC colon, ovarian, lung, head and neck, lymphoma, leukemia, melanoma, liver,  
CC gastric, kidney, bladder, pancreatic or endometrial cancer. The present  
CC sequence represents the lipophilin B polypeptide.

XX Sequence 90 AA;

Query Match 100.0%; Score 450; DB 22; Length 90;  
Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFEFISBPFLKSLAKFPAPPAVAKL 60  
DB 1 MKLSVCLLVTLALCCYQANAEFCPALVSELDFEFISBPFLKSLAKFPAPPAVAKL 60

QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 10  
 AA07518  
 ID AA07518 standard; Protein; 90 AA.  
 XX  
 AC AA07518;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human lipophilin B protein.  
 XX  
 KW Human; lipophilin B; cytosolic; vaccine; gene therapy; uteroglobin;  
 KM cancer; breast; ovary; prostate.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200158947-A1.  
 XX  
 PD 16-AUG-2001.  
 XX  
 PF 08-FEB-2001; 2001WO-US04439.  
 XX  
 PR 11-FEB-2000; 2000US-0183495.  
 XX  
 PR 28-JUN-2000; 2000US-0215735.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Carter D, Vedvick TS, Valleve-Douglas J, Houghton RL, Dillon DC;  
 XX  
 DR WPI: 2001-497069/54.  
 XX  
 DR N-PSDB; AAD13756.  
 XX  
 PT Novel isolated complex two lipophilin-like polypeptides linked by at  
 PT least one disulfide bond, used to treat or prevent breast, ovarian or  
 PT prostate cancer -  
 XX  
 PS Example 5; Page 72; 91pp; English.  
 XX  
 CC The invention relates to a complex comprising a lipophilin-like  
 CC polypeptide linked by at least one disulfide bond to a second  
 CC lipophilin-like polypeptide. Lipophilin-like protein are members of  
 CC uteroglobin superfamily. Lipophilin-like proteins are useful in the  
 CC preparation of vaccines. The complex containing lipophilin-like  
 CC proteins are useful for treating or preventing breast, ovarian or  
 CC prostate cancer. The complex is also used for determining the  
 CC presence or absence of cancer in a patient, or monitor the progress  
 CC of cancer in a patient. Lipophilin DNA is also useful in gene therapy.  
 CC The present sequence is human lipophilin B protein.  
 CC  
 SQ Sequence 90 AA;

Query Match 100.0%; Score 450; DB 22; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVCLLVLTALCCYQNAEFCPALVSELDFFISPLKSLAKDPPEAVAAKL 60  
 Db 1 MKISVCLLVLTALCCYQNAEFCPALVSELDFFISPLKSLAKDPPEAVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 11  
 AAB31681  
 ID AAB31681 standard; Protein; 90 AA.  
 XX  
 AC AAB31681;

XX 30-APR-2001 (first entry)  
 DT  
 XX An endometrial specific steroid binding factor II.  
 DE  
 XX Human; endometrial specific steroid binding factor; hESF; hESFI; hESFII;  
 KM hESFII; inflammation; asthma; rhinitis; cystic fibrosis; airway disease;  
 KM neoplasia; atopy; phospholipase A2; polychlorinated biphenyl; chemotaxis;  
 KM phagocytosis; platelet aggregation; eicosanoid; endometrial cell.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT  
 XX /note= "signal peptide"  
 XX  
 PN US6174992-B1.  
 XX  
 PD 16-JAN-2001.  
 XX  
 PF 08-MAR-1999; 99US-0263810.  
 XX  
 PR 21-MAR-1996; 96US-0014724.  
 XX  
 PR 21-MAR-1997; 97US-0821451.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI NI J, Yu G, Gentz R;  
 XX  
 DR WPI: 2001-158477/16.  
 XX  
 DR N-PSDB; AAF25213.  
 XX  
 PT New human endometrial specific steroid binding factors, useful for  
 PT treating and preventing inflammation, asthma, rhinitis, cystic  
 PT fibrosis, airway disease, neoplasia and atopy  
 XX  
 PS Claim 1; Fig 2; 36pp; English.  
 XX  
 CC The present sequence represents a human endometrial specific steroid  
 CC binding factor (hESF). The specification describes hESFI, hESFII, and  
 CC hESFIII. hESFI, II and III polypeptides, and polynucleotides encoding  
 CC them are useful for treating and preventing inflammation, asthma,  
 CC rhinitis, cystic fibrosis, airway disease, neoplasia and atopy,  
 CC inhibiting phospholipase A2 activity, binding polychlorinated  
 CC biphenyls, reducing foreign protein antigenicity, inhibiting monocyte  
 CC and neutrophil chemotaxis and phagocytosis, inhibiting platelet  
 CC aggregation, regulating eicosanoid levels in the human uterus, and for  
 CC controlling the growth of endometrial cells. hESF polypeptides and  
 CC nucleotides are also useful for research, biological, clinical or  
 CC therapeutic purposes.  
 CC  
 SQ Sequence 90 AA;

Query Match 100.0%; Score 450; DB 22; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKISVCLLVLTALCCYQNAEFCPALVSELDFFISPLKSLAKDPPEAVAAKL 60  
 Db 1 MKISVCLLVLTALCCYQNAEFCPALVSELDFFISPLKSLAKDPPEAVAAKL 60  
 QY 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90  
 Db 61 GVKRCTDQMSLQKRSLLAEVLVKILKCSV 90

RESULT 12  
 ABB09634  
 ID ABB09634 standard; Protein; 90 AA.  
 XX  
 AC ABB09634;  
 XX  
 DT 29-MAY-2002 (first entry)

XX Human endometrial specific steroid-binding factor (hESF) II.  
 DE Human: endometrial specific steroid-binding factor; ESF.  
 XX Prostatic steroid-binding protein; hESF I; hESF II; hESF III; asthma.  
 KW Homo sapiens.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /note= "signal peptide"  
 FT Protein 22..90  
 FT Protein /note= "mature protein"  
 PN US6338948-B1.  
 XX 15-JAN-2002.  
 PD 30-MAY-2000; 2000US-0583169.  
 PF 21-MAR-1996; 96US-014724P.  
 PR 21-MAR-1997; 97US-082145I.  
 PR 08-MAR-1999; 99US-0263810.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA NI J, Yu G, Gentz R;  
 PI WPI; 2002-215019/27.  
 DR N-PSDB; ABL1782.  
 XX New antibody specific for human endometrial specific steroid-binding  
 PT factor (hESF) III, useful for detecting hESF III protein in biological  
 PT sample and to isolate or identify clones expressing the protein -  
 XX Disclosure; Fig 1; 36pp; English.  
 PS  
 XX The present sequence represents a endometrial specific steroid-binding  
 CC factor (hESF) II. The full length protein has a molecular weight of  
 CC 9.9 kDa. The protein has homology to rat prostatic steroid-binding  
 CC protein C2. Antibodies which bind hESF proteins, such as hESF I, hESF II,  
 CC and hESF III are useful for isolating or to identify clones expressing  
 CC the polypeptides or to purify the polypeptides by affinity  
 CC chromatography. Agonists and antagonists of hESF proteins are useful  
 CC for treating and/or preventing susceptibility to asthma.  
 CC  
 SO Sequence 90 AA;  
 Query Match 100.0%; Score 450; DB 23; Length 90;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-51;  
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLYTALCCQANAERCPALVSELDFFIFSEPLFKLSLAKFPAPPAVAAKL 60  
 DB 1 MKLSVCLLYTALCCQANAERCPALVSELDFFIFSEPLFKLSLAKFPAPPAVAAKL 60  
 QY 61 GVKRCTDOMSLQKRSLLAEVLVILKKCSV 90  
 DB 61 GVKRCTDOMSLQKRSLLAEVLVILKKCSV 90  
 RESULT 13  
 ABB11907  
 ID ABB11907 standard; peptide; 117 AA.  
 AC ABB11907;  
 XX 11-JAN-2002 (first entry)  
 DT Human breast tumour-associated protein homologue, SPQ ID NO:2277.  
 DE Human: cytokine; cell proliferation; cell differentiation; growth factor;  
 XX haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW

KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antisthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytosolic; osteopathic; vasotropic; cardiatic; virucide; antibacterial;  
 KW antifungal; vulnereary; antilicer.  
 OS Homo sapiens.  
 PN WO200157188-A2.  
 XX 09-AUG-2001.  
 PD 05-FEB-2001; 2001WO-US03800.  
 PF 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 XX (HYSE-) HYSEQ INC.  
 PA Tang YT, Liu C, Drmanac RT;  
 PI WPI; 2001-457740/49.  
 DR N-PSDB; ABA09151.  
 XX Human proteins and DNA encoding sequences useful for preventing,  
 PT treating or ameliorating a medical condition in a mammalian subject  
 PT e.g. arthritis and cancer -  
 XX Claim 20; Page 275; 1963pp; English.  
 PS  
 XX Sequences ABB10981-ABB12330 represent 1150 novel human polypeptides, and  
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis, cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a novel human  
 CC polypeptide of the invention.

```

XX Sequence 117 AA:
SQ
Query Match 100.0%; Score 450; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
DB 28 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 87
OY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90
DB 88 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 117

RESULT 14
AAV48606
ID AAV48606 standard; Protein; 120 AA.
XX
AC AAV48606;
XX
DT 08-DEC-1999 (first entry)
XX
DE Human breast tumour-associated protein 67.
XX
KM Expressed sequence tag; EST; human; breast; cancer; gene therapy;
XX treatment; tumour; cytostatic; medicament.
XX
OS Homo sapiens.
XX
PN DE19813839-A1.
XX
PD 23-SEP-1999.
XX
PF 20-MAR-1998; 98DE-1013839.
XX
PR 20-MAR-1998; 98DE-1013839.
XX
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
XX
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;
DR WPI: 1999-528981/45.
DR N-PSDB; AA233666.
XX
PT Human nucleic acid sequences and protein products from tumor breast
PT tissue, useful for breast cancer therapy -
XX
PS Claim 22; 172; 188pp; German.
XX
CC This invention describes novel human nucleic acid sequences from tumor
CC breast tissue which have cytostatic activity. The nucleic acid sequences
CC can be used to produce and isolate full-length gene sequences. They can
CC be used to express proteins, which can be used as tools to find an
CC actively against breast cancer. The sequences can be used in sense or
CC antisense form. They are especially useful for medicaments for gene
CC therapy to treat breast cancer. AAV48540-Y48617 represent protein
CC fragments encoded by the expressed sequence tags described in the method
CC of the invention.
XX
SQ Sequence 120 AA:
Query Match 100.0%; Score 450; DB 20; Length 120;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
DB 31 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 90
OY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90

```

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DB 91 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 120

RESULT 15
AAE07521
ID AAE07521 standard; Protein; 90 AA.
XX
AC AAE07521;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human lipophilin B S11 3 3 protein.
XX
KM Human; lipophilin B S11 3 3; cytostatic; vaccine; gene therapy;
XX uteroglobin; cancer; breast; ovary; prostate.
XX
OS Homo sapiens.
XX
PN WO200158947-A1.
XX
PD 16-AUG-2001.
XX
PF 08-FEB-2001; 2001WO-US04439.
XX
PR 11-FEB-2000; 2000US-0183495.
XX
PR 28-JUN-2000; 2000US-0215735.
XX
PA (CORI-) CORIXA CORP.
XX
PI Carter D, Vedvick TS, Vailieve-Douglas J, Houghton RL, Dillon DC;
DR WPI: 2001-497069/54.
DR N-PSDB; AAD13761.
XX
PT Novel isolated complex two lipophilin-like polypeptides linked by at
PT least one disulfide bond, used to treat or prevent breast, ovarian or
PT prostate cancer -
XX
PS Example 5; Page 82; 91pp; English.
XX
CC The invention relates to a complex comprising a lipophilin-like
CC polypeptide linked by at least one disulfide bond to a second
CC lipophilin-like polypeptide. Lipophilin-like proteins are members of
CC uteroglobin superfamily. Lipophilin-like proteins are useful in the
CC preparation of vaccines. The complex containing lipophilin-like
CC proteins are useful for treating or preventing breast, ovarian or
CC prostate cancer. The complex is also used for determining the
CC presence or absence of cancer in a patient, or monitor the progress
CC of cancer in a patient. Lipophilin DNA is also useful in gene therapy.
CC The present sequence is human lipophilin B S11 3 3 protein.
XX
SQ Sequence 90 AA:
Query Match 99.3%; Score 447; DB 22; Length 90;
Best Local Similarity 98.9%; Pred. No. 2.3e-50;
Matches 89; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
DB 1 MKLSVCLLVLTALCCYQNAEFCPALVSELDFFFISEPLFKLSLAKFDAPPEAVAATL 60
OY 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90
DB 61 GVKRCTDQMSLQKRSLIAEVLVKILKCSV 90

Search completed: January 2, 2003, 14:54:21
Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:52:47 : Search time 12 Seconds

(without alignments)  
311.072 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450

Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLKILKCSV 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450	100.0	90	1	LPBP_HUMAN
2	267	59.3	90	1	LPBP_HUMAN
3	206	45.8	111	1	PSC1_RAT
4	171	38.0	112	1	PSC2_RAT
5	110	24.4	91	1	UTER_HUMAN
6	102	22.7	91	1	UTER_RABIT
7	101	22.4	96	1	UTER_MOUSE
8	100	22.2	91	1	UTER_LEPCA
9	100	22.2	96	1	UTER_RAT
10	80.5	17.9	139	1	UGRI_MOUSE
11	75.5	16.8	93	1	UGRI_HUMAN
12	69	15.3	144	1	CYF_MOUSE
13	66.5	14.8	3079	1	IRY4_YEAST
14	62.5	13.9	90	1	SYO2_CHICK
15	62	13.8	145	1	FEL2_FELCA
16	62	13.8	109	1	CYF_MOUSE
17	61.5	13.7	200	1	RISA_CHLPN
18	61	13.6	92	1	FELA_FELCA
19	60.5	13.4	1390	1	MET_HUMAN
20	60	13.3	123	1	CCN1_XENLA
21	59	13.1	261	1	YSC1_YERPE
22	59	13.0	270	1	ILIA_FELCA
23	58.5	13.0	646	1	GYR_MYCA
24	58.5	13.0	1078	1	CYR_BOVIN
25	58	12.9	140	1	FLAF_METJA
26	58	12.9	724	1	ME10_CAEL
27	57.5	12.8	95	1	PSC3_RAT
28	57.5	12.8	591	1	VATA_CHLPN
29	57	12.7	282	1	D1L_DICDI
30	57	12.7	441	1	YDW1_SCHPO
31	57	12.7	608	1	ALB1_SALSA
32	57	12.7	608	1	ALB2_SALSA
33	57	12.7	1107	1	YLR2_CAEL

34	56.5	12.6	137	1	VGIL_EBV
35	56.5	12.6	262	1	Y096_METJA
36	56.5	12.6	489	1	MONT_RAF
37	56.5	12.6	556	1	NU2M_PODAN
38	56.5	12.6	621	1	FX14_HUMAN
39	56.5	12.6	1080	1	CYAT_HUMAN
40	56	12.4	406	1	P152_HUMAN
41	56	12.4	446	1	AK_RICPR
42	56	12.4	1653	1	YFHM_ECOLI
43	55.5	12.3	76	1	RPOH_ARCFU
44	55.5	12.3	195	1	CNTE_CHICK
45	55.5	12.3	207	1	PLCR_PSEAE

## ALIGNMENTS

RESULT 1	ID	LPBP_HUMAN	STANDARD:	PRT:	90 AA.
AC	095969				
DT	30-MAY-2000 (Rel. 39, Created)				
DT	30-MAY-2000 (Rel. 39, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Lipophilin B precursor (Secretoglobulin family ID member 2).				
GN	SCGB1D2 OR LIPHB.				
OS	Homo sapiens (human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-99167354; PubMed-10066439;				
RA	Zhao C., Nguyen T., Yusifov T., Glasgow J.J., Lehrer R.I.,				
RT	"Lipophilins: human peptides homologous to rat prostactin.";				
RL	Biochem. Biophys. Res. Commun. 256:147-155(1999).				
CC	-1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS. MAY ALSO BIND				
CC	ESTRADIOL. A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER.				
CC	MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.				
CC	-1- SUBCELLULAR LOCATION: Secreted (potential).				
CC	-1- TISSUE SPECIFICITY: HIGHEST EXPRESSION WAS FOUND IN SKELETAL				
CC	MUSCLE. EXPRESSED AS WELL IN THYMUS, TRACHEA, KIDNEY, STEROID				
CC	RESPONSIVE TISSUES (PROSTATE, TESTIS, UTERUS, BREAST AND OVARY),				
CC	AND SALIVARY GLAND.				
CC	-1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN				
CC	SUBFAMILY.				
CC	-----				
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
DR	EMBL: AJ224172; CA11864.1; -				
DR	Genev; HGNC:18396; SCGB1D2.				
DR	InterPro: IPR000329; Uterogloblin.				
DR	Pfam: PF01099; Uterogloblin; 1.				
DR	PRINTS: PRO0486; UTEROGLOBIN.				
DR	SMART: SM00096; UTG; 1.				
KW	Signal.				
FT	SIGNAL	1	21	POTENTIAL.	
FT	CHAIN	22	90	LIPOPHILIN B.	
FT	SEQUENCE	90 AA;	9925 MW;	17BB555ED035D1AF CRC64;	
QY	Query Match	100.0%;	Score 450;	DB 1;	Length 90;
QY	Best Local Similarity	100.0%;	Pred. No. 6.7e-45;		
QY	Matches	90;	Conservative	0;	Mismatches 0;
QY				Indels	0;
QY				Gaps	0;
Db	1 MKLSVCLLVTLALCCYQANAEPALVSELDFFFTSEPLFKLSLAKFPDAPPAVAKL 60				
Db	1 MKLSVCLLVTLALCCYQANAEPALVSELDFFFTSEPLFKLSLAKFPDAPPAVAKL 60				

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OY      61 GVKRCTDQMSLQKRSLIAEVLVKILKKCSV 90
          |||||
DB      61 GVKRCTDQMSLQKRSLIAEVLVKILKKCSV 90
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RESULT 2	
LPPA_HUMAN	
ID	LPPA_HUMAN
STANDARD;	PRT; 90 AA

DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE L1pophilin A precursor (Secretoglobin family ID member 1).  
DN SCGB1D1 OR L1PHA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId:9606;  
RN [1]  
RP  
RX MEDLINE=99167354; PubMed=1006439;  
RA Zhao C., Nguyen T., Yustifov T., Glasgow B.J., Lehrer R.I.;  
RT "L1pophilin: human peptides homologous to rat prostatein.";  
RL Biochem. Biophys. Res. Commun. 256:147-155(1999).  
173

CC RA GHOSWARI, B.J.:  
RT "Lipophilin," a novel heterodimeric protein of human tears.";  
RL FEBS Lett. 432:163-167(1998)  
CC -1- FUNCTION: MAY BIND ANDROGENS AND OTHER STEROIDS, MAY ALSO BIND  
CC ESTRAMUSTINE, A CHEMOTHERAPEUTIC AGENT USED FOR PROSTATE CANCER  
CC MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.  
CC -1- SUBUNIT: HETERODIMER OF A LIPOPHILIN A AND A LIPOPHILIN C  
CC (MAMMOGLOBIN B) MONOMER ASSOCIATED HEAD TO HEAD.  
CC CC -1- SUBCELLULAR LOCATION: Secreted (potential).  
CC CC -1- TISSUE SPECIFICITY: EXPRESSED IN LACRIMAL GLAND, THYMUS, KIDNEY,  
CC TESTIS, OVARY AND SALIVARY GLAND.  
CC CC -1- MASS SPECTROMETRY: MW=7574.69; METHOD-Electrospray; RANGE=22-90  
CC CC -1- SIMILARITY: BELONGS TO THE UBERGLOBLIN FAMILY. LIPOPHILIN  
CC SUBFAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC  
-----  
DR EMBL; AJ224171; CAA11863.1; -  
DR Genew; HGNC:18395; SCGB1d1.  
DR InterPro; IPR000329; Uteroglobin.  
DR Pfam; PF01099; Uteroglobin; 1.  
DR PRINTS; PR00486; UTEROglobin.  
DR SMART; SM00096; UTG; 1.

KW	Signal.	1	21	LIPOPHILIN A.	
FT	SIGNAL	22	90	FT2FD4F7565A87D34	CRC64;
FT	CHAIN	90	9898	MM;	
SO	SEQUENCE	90	AA;		
	Query Match		59.3%;	Score 267;	DB 1; Length 90;
	Best Local Similarity		60.2%;	Pred. No. 6.8e-24;	
	Matches 53; Conservative		12;	Mismatches 23;	Indels 0; Gaps 0;

QY 1 MKLSVCLLTVTALCCYOANNEPCPAIVSELIDEEFISEPLFKLSLAKFPDAPPEAVAAKL 60  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 1 MRLSVCLLTITLALCCYANNAVCOALSEITGLFLAGPVKFOIAKFAPLEAANAAM 60  
  
QY 61 GVKRCTDOMSLQKRSLIAEVLVKILKKC 88  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 61 EVKKCVDTMAYEKRLITKTLGIAEC 88

RESULT 3		
PSCI_RAT		
ID	PSCI_RAT	STANDARD;
00000000	00000000	PRT; 111 AA

DT 21-JUN-1986 (Rel. 01, Created)  
DT 13-AUG-1987 (Rel. 05, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Prostatic steroid-binding protein C1 chain precursor (Prostatein  
peptide C1).  
OS *Rattus norvegicus* (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82220075; PubMed=6896362;  
RA Parker M.G., Needham M., White R.;  
RT "Prostatic steroid binding protein: gene duplication and steroid  
binding".  
RL Nature 298:92-94(1982).

RN 12  
 RP REVISIONS.  
 RA Parker M.G.;  
 RL Submitted (JUL-1983) to the EMBL/GenBank/DBJ databases.  
 RN 13  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83234456; PubMed=6688048;  
 RA Delaey B., Dirckx I., Peeters B., Volckaert G., Mous J., Heyns W.,  
 RA Rombauts W.;  
 RT "The nucleotide sequence of cDNA complementary to the C1 component of  
 RL rat prostatic binding protein.".  
 Eur. J. Biochem. 133:645-649(1983).

RN [4]  
RP SEQUENCE OF 24-111.  
RX MEDLINE=82164744; Pubmed=200013;  
RA Peeters B., Heyns W., Mous J., Rombaux W.;  
RT "Structural studies on rat prostatic binding protein. The primary  
RL structure of component C1 from subunit F.";  
    Eur. J. Biochem. 123:55-62(1982).  
RN [5]  
RP SEQUENCE OF 24-111.  
RX MEDLINE=62075873; Pubmed=7198120;  
RA Liao S., Chen C., Huang I.-Y.;  
RT "Prostate alpha-protein. Complete amino acid sequence of the  
RL component that inhibits nuclear retention of the androgen-receptor  
    protein complex.";  
    J. Biol. Chem. 257:122-125(1982).

RN 16] SEQUENCE OF 13-65 FROM N.A.  
 RP Deaey B., Rombaux W., Volckaert G., Peeters B., Heys W.;  
 RA "Identification of a complementary-DNA clone containing part of the  
 RT "identification of a complementary-DNA clone containing part of the  
 RT protein information for the C-1-polypeptide of rat prostatic blinding  
 RT protein.";  
 RL Biochem. Soc. Trans. 10:51-51(1982).  
 CC -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY  
 CC GLYCOPROTEIN OF VENTRAL PROSTATIC GLAND.  
 CC -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED  
 CC C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)  
 CC HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC  
 CC (C1:C3/C3:C2) PROSTATEIN MOLECULES.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MISCELLANEOUS: THE HETERODIMER CAN BIND NON-POLAR STEROIDS,  
 CC CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPILIN  
 CC SUBFAMILY.

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**CC** -1- FUNCTION: PART OF PROSTATEIN WHICH IS THE MAJOR SECRETORY  
**CC** GLYCOPROTEIN OF VENTRAL PROSTATE GLAND.  
**CC** -1- SUBUNIT: PROSTATEIN IS COMPOSED OF THREE DIFFERENT PEPTIDES CALLED  
**CC** C1, C2 AND C3. THESE FORM COVALENT C1:C3 (F) AND C2:C3 (S)  
**CC** HETERODIMERS WHOSE NONCOVALENT ASSOCIATION FORMS TETRAMERIC  
**CC** (C1:C3/C3:C2) PROSTATEIN MOLECULES.  
**CC** -1- SUBCELLULAR LOCATION: Secreted.  
**CC** -1- PTM: LINKED BY THREE DISULFIDE BONDS TO C3.  
**CC** -1- MISCELLANEOUS: THE HETERODIMER CAN BIND NON-POLAR STEROIDS,  
**CC** CHOLESTEROL AND A GROUP OF SMALL PROLINE-RICH PEPTIDES.  
**CC** -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. LIPOPHILIN  
**CC** SUBFAMILY.

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**DR** EMBL; X05034; CAAB8708.1; -.  
**DR** EMBL; V01256; CAAB24569.1; -.  
**DR** EMBL; J00776; AAA51641.1; -.  
**DR** PIR; A03251; B0R72.  
**DR** PIR; A26671; A26671.  
**DR** InterPro; IPR000329; Uteroglobin.  
**DR** ProSITE; PS00403; UTEROGLOBIN\_1; FALSE\_NING.  
**KW** PROSITE; PS00404; UTEROGLOBIN\_2; FALSE\_NING.  
**FT** Steroid-binding; Signal.  
**FT** SIGNAL 1 20  
**FT** CHAIN 21 112  
**FT** MOD\_RES 21 21 BLOCKED.  
**FT** DISULFID 28 26 INTERCHAIN (WITH C3) (PROBABLE).  
**FT** DISULFID 69 69 INTERCHAIN (WITH C3) (PROBABLE).  
**FT** DISULFID 92 92 INTERCHAIN (WITH C3) (PROBABLE).  
**FT** CONFLICT 26 26 MISSING (IN REF. 3).  
**FT** CONFLICT 88 88 I -> T (IN REF. 3).  
**FT** CONFLICT 96 112 VWLIQNPGRGAFPSFIN -> YGYK (IN REF. 3).  
**SQ** SEQUENCE 112 AA; 12828 MW; DA65A6A8E677864 CAC64;

---

**Query Match** 38.0%; Score 171; DB 1; Length 112;  
**Best Local Similarity** 42.1%; Pred. No. 8.8e-13;  
**Matches** 40; Conservative 13; Mismatches 36; Indels 6; Gaps 2;

<b>OY</b> 1 MKLSVCLLVLTALACCYYOAN-----AEFCPALVSFLDDFFTSSEPLFKSLAKDPAPPEA 55  ::  :: :- -  :: :-   <b>Dy</b> 1 MRISLCILLTI-LVVCCANGOTLAGOVCAOLDVTIFLLNPEELKRRELFEPAPPEA 59  ::    :: :- -  :: :-   <b>OY</b> 56 VAAKGVKRCCTDOMSIQRSLIAEVLYTKLKCSY 90           ::  :-  :  :  :  :  :  <b>Dy</b> 60 VEANIKYRKCIINKIMYGRLSMGSTVLFIMLKCV 94           ::  :-  :  :  :  :  :	RESULT 5 UTHER_HUMAN STANDARD: PROT: 9..AA. ID UTHER_HUMAN STANDARD: AC P11684; O9UCM4; O9UCM2; DT 01-OCT-1989 (Rel. 12, Created) DT 01-OCT-1989 (Rel. 12, Last sequence update) DT 15-JUN-2002 (Rel. 41, Last annotation update) DE Clara cell phospholipid-binding protein precursor (CCBPp) (Clara cells DE 10 kDa secretory protein) (CC10) (Uteroglobin) (Urline protein 1) DN (UPI1) GN SCGB1A1 OR USB OR CC10 OR CCSP. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. OX NCBI_TaxId=9606; RN [1] RP SEQUENCE FROM N.A. RC TISSUE=Lung;
--	--

RX MEDLINE=89000784; PubMed=3167058;  
 RA Singh G., Katyal S.L., Brown W.E., Phillips S., Kennedy A.L.,  
 RA Anthony J., Squeglia N.;  
 RT "Amino-acid and cDNA nucleotide sequences of human Clara cell 10 kDa  
 RT protein."; Biochem. Biophys. Acta 950:329-337(1988).  
 RL Bioclin. Biophys. Acta 950:329-337(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=95250987; PubMed=7733299;  
 RA Hay J.G., Danel C., Chu C., Crystal R.G.;  
 RT "Human CC10 gene expression in airway epithelium and subchromosomal  
 RT locus suggest linkage to airway disease."; Am. J. Physiol. 268:L565-L575(1995).  
 RL [3]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Pancreas;  
 RA Strusberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-18 FROM N.A.  
 RX MEDLINE=93250776; PubMed=1284526;  
 RA Wolf M., Klug J., Hackenberg R., Gessler M., Grzeschik K.-H.,  
 RA Beato M., Suske G.;  
 RT "Human CC10, the homologue of rabbit uteroglobin: genomic cloning,  
 RT chromosomal localization and expression in endometrial cell lines."; Hum. Mol. Genet. 1:371-378(1992).  
 RL [5]  
 RN SEQUENCE OF 22-74.  
 RP TISSUE=urine;  
 RX MEDLINE=93016476; PubMed=1400743;  
 RA Okutani R., Itoh Y., Hirata H., Kasahara T., Mukaida N., Kawai T.;  
 RT "Simple and high-yield purification of urine protein 1 using  
 RT immunofluorescence chromatography: evidence for the identity of urine  
 RT protein 1 and human Clara cell 10-kilodalton protein."; J. Chromatogr. A 577:25-35(1992).  
 RL [6]  
 RN SEQUENCE OF 22-45.  
 RP TISSUE=urine;  
 RX MEDLINE=93009001; PubMed=1395029;  
 RA Bernard A., Roels H., Lauwers R., Witters R., Gielens C.,  
 RA Sunmullion A., Van Damme J., De Ley M.;  
 RT "Human urinary protein 1: evidence for identity with the Clara cell  
 RT protein and occurrence in respiratory tract and urogenital  
 RT secretions."; Clin. Chim. Acta 207:239-249(1992).  
 RL [7]  
 RN SEQUENCE OF 22-33.  
 RP MEDLINE=21648993; PubMed=11788998;  
 RA Chafouri B., Stahlbom B., Tagesson C., Lindahl M.;  
 RT "Newly identified proteins in human nasal lavage fluid from  
 RT non-smokers and smokers using two-dimensional gel electrophoresis and  
 RT peptide mass fingerprinting."; Proteomics 2:112-120(2002).  
 RL [8]  
 RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
 RX MEDLINE=95393197; PubMed=7664082;  
 RA Umland T.C., Swaminathan S., Singh G., Warty V., Furey W.,  
 RA Pletcher J., Sax M.;  
 RT "Structure of a human Clara cell phospholipid-binding protein-ligand  
 RT complex at 1.9-A resolution."; Nat. Struct. Biol. 1:538-545(1994).  
 RL [9]  
 RN -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,  
 CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT  
 CC INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -1- SUBUNIT: Homodimer: antiparallel disulfide-linked.  
 CC -1- TISSUE SPECIFICITY: CLARA CELLS (NONCILIATED CELLS OF THE  
 CC SURFACE EPITHELIUM OF THE PULMONARY AIRWAYS).  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLIBIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X13197; CAA31584.1; -  
 DR EMBL: U01101; AAA81885.1; -  
 DR EMBL: U01102; AAA18297.1; -  
 DR EMBL: BC004481; AAA04481.1; -  
 DR EMBL: X59875; CAA42532.1; -  
 DR PIR: J50036; J50036.  
 DR PIR: S2651; S2651.  
 DR HSSP: P02779; 1UNG.  
 DR GeneW: HGNC:12523; SCGB1A1.  
 DR MIM: 192020; -  
 DR InterPro: IPR003628; Uteroglbn\_sub.  
 DR InterPro: IPR000329; Uteroglbn.  
 DR Pfam: PF01099; Uteroglbn.1.  
 DR PRINTS: PR00486; UTEROGLIBIN.  
 DR ProDom: PD012475; Uteroglbn\_sub; 1.  
 DR SMART: SM00096; UMG; 1.  
 DR PROSITE: PS00403; UTEROGLIBIN\_1; 1.  
 DR PROSITE: PS00404; UTEROGLIBIN\_2; 1.  
 DR Phospholipase A2 inhibitor; Signal; Polymorphism.  
 KW SIGNAL 1 21  
 FT CHAIN 1 22 91 CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.  
 FT DISULFID 24 24 INTERCHAIN (WITH C-90').  
 FT DISULFID 90 90 INTERCHAIN (WITH C-24').  
 FT VARIANT 56 56 R -> G (IN DBSNP:1802634).  
 FT VARIANT 68 68 /FTID=VAR\_012045.  
 FT VARIANT 68 68 T -> A (IN DBSNP:1802632).  
 FT CONFLICT 24 24 /FTID=VAR\_012046.  
 FT FT C -> E (IN REF. 7).  
 SQ SEQUENCE 91 AA; 9994 MW; FE65AC678F12ABD CRC64;  
 Query Match 24.4%; Score 110; DB 1; Length 91;  
 Best Local Similarity 31.0%; Pred. No. 7; 1e-06;  
 Matches 26; Conservative 17; Mismatches 41; Indels 0; Gaps 0;  
 QY 1 MKLSYCLLVLTALCCYQNAEFCPALVSELDFFISPLKLSIAKDPAPPAVAKL 60  
 DB 1 MRLAVTLTTLTALCCSSAELICSPQVRIETLMDPTSSYEAMNELSPQDPRRNGA 60  
 QY 61 GVKRCTQMSLQKSLIAEVLKI 84  
 DB 61 QLKIVDTLPQKPRESTIKIMEKI 84  
 RESULT 6  
 UTER\_RABBIT  
 ID UTER\_RABBIT STANDARD; PRT; 91 AA.  
 AC P02779;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Uteroglobin precursor (Blastokinin).  
 GN SCGB1A1 OR UGB OR UGL.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_Taxid=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83290960; PubMed=6309802;  
 RA Bailey A., Atger M., Atger P., Cerdon M.-A., Allison M., Vu Hai M.T.,  
 RA Logeat F., Milgrom E.;  
 RT "The rabbit uteroglobin gene. Structure and interaction with the  
 RT progesterone receptor."; J. Biol. Chem. 258:10384-10389(1983).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=83220783; PubMed=6304644;  
 RA Suske G., Wenz M., Cato A.C.B., Beato M.;



RT "The uteroglobin gene region: hormonal regulation, repetitive  
 RT elements and complete nucleotide sequence of the gene.";  
 RL Nucleic Acids Res. 11:2257-2271(1983).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83014990; PubMed-6956897;  
 RA Menne C., Suske G., Arnenann J., Menz M., Cato A.C.B., Beato M.;  
 RT "Isolation and structure of the gene for the progesterone-inducible  
 RT protein uteroglobin.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 79:4853-4857(1982).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-83157105; PubMed-6299663;  
 RA Chandra T., Bullock D.W., Moo S.L.C.;  
 RT "Hormonally regulated mammalian gene expression: steady-state level  
 RT and nucleotide sequence of rabbit uteroglobin mRNA.";  
 RL DNA 1:19-26(1981).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-82275176; PubMed-6287481;  
 RA Suske G., Menne C., Cato A., Wenz M., Beato M.;  
 RT "Characterization and sequence analysis of interspersed repetitive  
 RT DNA sequences transcribed in X. laevis embryos.";  
 RL Prog. Clin. Biol. Res. 85:139-146(1982).  
 RN [6]  
 RP SEQUENCE OF 1-73.  
 RX MEDLINE-79187160; PubMed-571719;  
 RA Atger M., Mercier J.-C., Haze G., Fridlansky F., Milgrom E.;  
 RT "N-terminal sequences of uteroglobin and its precursor.";  
 RL Biochem. J. 177:985-988(1979).  
 RN [7]  
 RP SEQUENCE OF 22-91.  
 RX MEDLINE-79042086; PubMed-568483;  
 RA Ponstingl H., Nieto A., Beato M.;  
 RT "Amino acid sequence of progesterone-induced rabbit uteroglobin.";  
 RL Biochemistry 17:3908-3912(1978).  
 RN [8]  
 RP SEQUENCE OF 22-91.  
 RX MEDLINE-79074850; PubMed-281700;  
 RA Popp R.A., Foresman K.R., Wise L.D., Daniel J.C. Jr.;  
 RT "Amino acid sequence of a progesterone-binding protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 75:5516-5519(1978).  
 RN [9]  
 RP REVISIONS TO 50-62 AND 67-71.  
 RA Popp R.A., Foresman K.R., Wise L.D., Daniel J.C. Jr.;  
 RT Submitted (OCT-1982) to the PIR data bank.  
 RN [10]  
 RP SEQUENCE OF 22-91 FROM N.A.  
 RX MEDLINE-86056319; PubMed-2415398;  
 RA de Haro M.S., Nieto A.;  
 RT "Primary structure of rabbit lung uteroglobin as deduced from the  
 RT nucleotide sequence of a cDNA.";  
 RL FEBS Lett. 193:247-249(1985).  
 RN [11]  
 RP SEQUENCE OF 39-77 FROM N.A.  
 RX MEDLINE-81021016; PubMed-7417250;  
 RA Chandra T., Moo S.L.C., Bullock D.W.;  
 RT "Cloning of the rabbit uteroglobin structural gene.";  
 RL Biochem. Biophys. Res. Commun. 95:197-204(1980).  
 RN [12]  
 RP SEQUENCE OF 53-72 FROM N.A.  
 RX MEDLINE-80241888; PubMed-6156676;  
 RA Atger M., Perricaudet M., Tjollia P., Milgrom E.;  
 RT "Bacterial cloning of the rabbit uteroglobin structural gene.";  
 RL Biochem. Biophys. Res. Commun. 93:1082-1088(1980).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (1.64 ANGSTROMS).  
 RX MEDLINE-89199637; PubMed-2704039;  
 RA Bally R., Delettre J.;  
 RT "Structure and refinement of the oxidized P21 form of uteroglobin at  
 RT 1.64 Å resolution.";  
 RL J. Mol. Biol. 206:153-170(1989).  
 RN [14]

RP X-RAY CRYSTALLOGRAPHY (1.34 ANGSTROMS).  
 RX MEDLINE-88011213; PubMed-3656405;  
 RA Morize I., Surcouf E., Vaney M.C., Epeiboin Y., Buehner M.,  
 RA Fridlansky F., Milgrom E., Moron J.-P.;  
 RT "Refinement of the C222(1) crystal form of oxidized uteroglobin at  
 RT 1.34-Å resolution.";  
 RL J. Mol. Biol. 194:725-739(1987).  
 RN [15]  
 RP STRUCTURE BY NMR OF 39-68  
 RX MEDLINE-94297152; PubMed-8025221;  
 RA Imprita S., Pastore A., Mammì S., Peggion E.;  
 RT "Conformation and molecular dynamics calculations on uteroglobin  
 RT fragment 18-47.";  
 RL Biopolymers 34:773-782(1994).  
 CC -1- FUNCTION: UTEROGLIBIN BINDS PROGESTERONE SPECIFICALLY AND WITH  
 CC HIGH AFFINITY. IT MAY REGULATE PROGESTERONE CONCENTRATIONS  
 CC REACHING THE BLATOCYST. IT IS ALSO A POTENT INHIBITOR OF  
 CC PHOSPHOLIPASE A2.  
 CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.  
 CC -1- INDUCTION: UTEROGLIBIN, SYNTHESIZED IN THE UTERUS AND LUNG, IS  
 CC SECRETED BY THE UTERUS UPON INDUCTION BY PROGESTERONE.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLIBIN FAMILY.  
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 CC -----  
 DR EMBL: K01657; AAA31497.1; -;  
 DR EMBL: J00689; AAA31495.1; -;  
 DR EMBL: J00688; AAA31495.1; JOINED.  
 DR EMBL: X01423; CAA25669.1; -;  
 DR EMBL: M32012; AAA31500.1; -;  
 DR EMBL: M25090; AAA31500.1; JOINED.  
 DR EMBL: M27564; AAA31496.1; -;  
 DR EMBL: M25057; AAA31498.1; -;  
 DR EMBL: M25038; AAA31499.1; -;  
 DR PIR: A03249; UGRB.  
 DR PDB: 1UTG; 15-OCT-92.  
 DR PDB: 2UTG; 15-OCT-89.  
 DR InterPro: IPR003628; Uteroglbn sub.  
 DR InterPro: IPR000329; Uteroglbn.  
 DR Pfam: PF01099; Uteroglbn.1.  
 DR PRINTS: PR00486; UTEROGLIBIN.  
 DR PRODOM: PD012475; Uteroglbn\_sub; 1.  
 DR SMART: SM00096; UTG; 1.  
 DR PROSITE: PS00403; UTEROGLIBIN\_1; 1.  
 DR PROSITE: PS00404; UTEROGLIBIN\_2; 1.  
 KW Phospholipase A2 inhibitor; Steroid-binding; Signal; 3D-structure.  
 FT STGNAL 1 21  
 FT CHAIN 22 91  
 FT DISULFID 24 24  
 FT DISULFID 90 90  
 FT CONFLICT 6 6  
 FT CONFLICT 16 16  
 FT CONFLICT 46 46  
 FT CONFLICT 67 68  
 FT CONFLICT 82 82  
 FT HELIX 25 36  
 FT HELIX 39 47  
 FT TURN 48 49  
 FT TURN 53 66  
 FT TURN 67 68  
 FT TURN 71 85  
 FT HELIX 86 86  
 FT TURN 88 90  
 FT HELIX 91 91  
 SO SEQUENCE 91 AA; 9983 MW; 0C1978A8A15D550CA CRC64;  
 Query Match 22.7%; Score 101; DB 1; Length 91;  
 Best Local Similarity 30.2%; Pred. No. 5,9e-05;



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 CC -----  
 DR EMBL: M25609; AAA30960.1; -  
 DR PIR: A23825; UGRBL.  
 DR HSSP: P02779; UTRG.  
 DR InterPro: IPR003628; Uteroglobn\_sub.  
 DR InterPro: IPR000329; Uteroglobln.  
 DR Pfam: PF01099; Uteroglobln.1.  
 DR PRINTS: PR00486; UTEROGLOBIN.  
 DR ProDom: PD012475; Uteroglobn\_sub; 1.  
 DR SMART: SM00096; UTRG; 1.  
 DR PROSITE: PS00403; UTEROGLOBIN.1; 1.  
 DR PROSITE: PS00404; UTEROGLOBIN.2; 1.  
 DR Phospholipase A2 inhibitor; Steroid-binding; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 91 UTEROGLOBIN.  
 FT DISULFID 24 24 INTERCHAIN (WITH C-90').  
 FT DISULFID 90 90 INTERCHAIN (WITH C-24').  
 SQ SEQUENCE 91 AA; 9879 MW; 587614DAE9E4820F CRC64;  
 Query Match 22.2%; Score 100; DB 1; Length 91;  
 Best Local Similarity 30.2%; Pred. No. 0.0001;  
 Matches 26; Conservative 16; Mismatches 44; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVLTALACQYANAEFCPALVSELDFFISSEPLFKSLAKDAPAEVAARL 60  
 DB 1 MKLTITLVLTALACSPASAGCPCFAHVIEMLLGTSSVTSLEKQPPDAMDAGM 60  
 QY 61 GYKRCTDMSLQKRSLLAEVLYKILK 86  
 DB 61 OMKRVLDLPQTRRENIIRLTERIKV 86  
 RESULT 9  
 UTR-RAT STANDARD; PRT; 96 AA.  
 AC P17559;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Clara cell phospholipid-binding protein precursor (CCBP) (Clara cells  
 DE 10 kDa secretory protein) (CC10) (Uteroglobln) (PCB-binding protein).  
 GN SCGB1A1 OR UGB OR CC10 OR UTRG.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RX MEDLINE=90324266; PubMed=2115524;  
 RA Nordlund-Moeller L., Andersson O., Ahlgren R., Schilling J.,  
 RA Gillner M., Gustafsson J.-A., Lund J.;  
 RA "Cloning, structure, and expression of a rat binding protein for  
 RA polychlorinated biphenyls. Homology to the hormonally regulated  
 RA progesterone-binding protein uteroglobln.";  
 RL J. Biol. Chem. 265:12690-12693(1990).  
 RN [3]  
 RP SEQUENCE OF 1-18 FROM N.A.  
 RX MEDLINE=9072398; PubMed=2349092;  
 RA Hagen G., Wolf M., Katyal S.L., Singh G., Beato M., Suske G.;

RT "Tissue-specific expression, hormonal regulation and 5'-flanking gene  
 RT region of the rat Clara cell 10 kDa protein: comparison to rabbit  
 RT uteroglobln.";  
 RL Nucleic Acids Res. 18:2939-2946(1990).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE=92219263; PubMed=1560460;  
 RA Umland T.C., Swaminathan S., Furey W., Singh G., Pletcher J., Sax M.;  
 RT "Refined structure of rat Clara cell 17 kDa protein at 3.0-A  
 RT resolution.";  
 RL J. Mol. Biol. 224:441-448(1992).  
 RN [5]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=96069785; PubMed=7583672;  
 RA Haerd T., Barnes H.J., Larsson C., Gustafsson J.-A., Lund J.;  
 RT "Solution structure of a mammalian PCB-binding protein in complex  
 RT with a PCB.";  
 RL Nat. Struct. Biol. 2:983-989(1995).  
 CC -1- FUNCTION: BINDS PHOSPHATIDYLCHOLINE, PHOSPHATIDYLINOSITOL,  
 CC POLYCHLORINATED BIPHENYLS (PCB) AND WEAKLY PROGESTERONE, POTENT  
 CC INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -1- SUBUNIT: Homodimer; antiparallel disulfide-linked.  
 CC -1- TISSUE SPECIFICITY: CLARA CELLS (NON-ILATED CELLS OF THE  
 CC SURFACE EPITHELIUM OF THE PULMONARY AIRWAYS).  
 CC -1- INDUCTION: BY GLUCOCORTICOIDS.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: J05536; AAA1817.1; -  
 DR EMBL: X51318; CAA35701.1; -  
 DR PIR: A36581; A36581.  
 DR PIR: S10185; A10185.  
 DR PIR: S21676; S21676.  
 DR PDB: 1CCD; 31-JAN-94.  
 DR PDB: 1CTR; 07-DEC-95.  
 DR InterPro: IPR003628; Uteroglobn\_sub.  
 DR InterPro: IPR000329; Uteroglobln.  
 DR Pfam: PR00486; UTEROGLOBIN.1.  
 DR PRINTS: PR00486; UTEROGLOBIN.  
 DR ProDom: PD012475; Uteroglobn\_sub; 1.  
 DR SMART: SM00096; UTRG; 1.  
 DR PROSITE: PS00403; UTEROGLOBIN.1; 1.  
 DR PROSITE: PS00404; UTEROGLOBIN.2; 1.  
 KW Phospholipase A2 inhibitor; Signal; 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 96  
 FT DISULFID 24 24 CLARA CELL PHOSPHOLIPID-BINDING PROTEIN.  
 FT DISULFID 90 90 INTERCHAIN (WITH C-90').  
 FT TURN 21 22 INTERCHAIN (WITH C-24').  
 FT HELIX 25 34  
 FT TURN 35 36  
 FT HELIX 39 46  
 FT TURN 47 49  
 FT HELIX 53 68  
 FT HELIX 71 84  
 FT TURN 85 86  
 FT TURN 88 90  
 SQ SEQUENCE 96 AA; 10449 MW; 1A13988677B9EBEF CRC64;  
 Query Match 22.2%; Score 100; DB 1; Length 96;  
 Best Local Similarity 25.9%; Pred. No. 0.00011;  
 Matches 22; Conservative 22; Mismatches 41; Indels 0; Gaps 0;  
 QY 1 MKLSVCLLVLTALACQYANAEFCPALVSELDFFISSEPLFKSLAKDAPAEVAARL 60  
 DB 1 MKLTITLVLTALACSPASAGCPCFAHVIEMLLGTSSVTSLEKQPPDAMDAGM 60

OY 61 GVKRCTDMSLOKRSLIAEVLVKIL 85  
 DB 61 QLRKLVDTLPOETRINIVKLFREKIL 85

# RESULT 10

UGR1\_MOUSE STANDARD: PRT: 139 AA.  
 ID UGR1\_MOUSE  
 AC Q920H1: Q920H2: Q920H3:  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).  
 GN SCGB3A2 OR UGRP1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539178; PubMed=11682631;  
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;  
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";  
 RL Mol. Endocrinol. 15:2021-2036(2001).  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; A, B and C (shown here); are produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. UGRP SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AF274959; AAL25708.1; -  
 CC EMBL: AF274960; AAL25709.1; -  
 CC EMBL: AF274961; AAL25710.1; -  
 CC InterPro: IPR000329; Uteroglobin.  
 CC Pfam: PF01099; Uteroglobin; 1.  
 CC Signal; Alternative splicing.  
 CC SIGNAL 1 21 POTENTIAL.  
 CC CHAIN 1 21 UTEROGLOBIN-RELATED PROTEIN 1.  
 CC FT 22 139 VSFLPMICAYPRDSKQTFATFERVEQSKL -> EALS  
 CC FT 107 139 HLV (IN ISOFORM B).  
 CC FT VARSPLIC 107 139 VTIICSY -> EALSHLY (IN ISOFORM A).  
 CC FT VARSPLIC 85 91 MISSING (IN ISOFORM A).  
 CC FT VARSPLIC 92 139  
 CC FT SEQUENCE 139 AA; 15431 MW; 8A2FB08DBA1E55E4 CRC64;

Query Match 17.9%; Score 80.5; DB 1; Length 139;  
 Best Local Similarity 27.6%; Pred. No. 0.027;  
 Matches 27; Conservative 19; Mismatches 35; Indels 17; Gaps 5;

OY 1 MKLSVCLLVTLALCCYQANA-----EFCPALVSELDFFFISEPLFKLSLAKFDA 51  
 DB 1 MKLVSIFLLVITIGICYSATALLINRLPVDKLPVPLDILIPSF---DPL-KMLKTIGI 56  
 OY 52 PPEAVAAKLGVKRCTDMSLOKRSLIAEVLVKILKKS 89  
 DB 57 SVEHLVLT--GLKRCVDELGPASEAVKRLVLI--CS 90

RESULT 11

UGR1\_HUMAN STANDARD: PRT: 93 AA.  
 ID UGR1\_HUMAN  
 AC Q96P11:  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).  
 GN SCGB3A2 OR UGRP1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21539178; PubMed=11682631;  
 RA Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;  
 RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";  
 RL Mol. Endocrinol. 15:2021-2036(2001).  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung.  
 CC -1- SIMILARITY: BELONGS TO THE UTEROGLOBIN FAMILY. UGRP SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AF313455; AAL26215.1; -  
 CC Genew: HGNC:18391; SCGB3A2.  
 CC MIM: 606531; -  
 CC Signal.  
 CC SIGNAL 1 21 POTENTIAL.  
 CC CHAIN 22 93 UTEROGLOBIN-RELATED PROTEIN 1.  
 CC FT SEQUENCE 93 AA; 10161 MW; FB4BFRAC2BF3718 CRC64;

Query Match 16.8%; Score 75.5; DB 1; Length 93;  
 Best Local Similarity 27.0%; Pred. No. 0.067;  
 Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

OY 1 MKLSVCLLVTLALCCYQANA-----EFCPALVSELDFFFISEPLFKLSLAKF 49  
 DB 1 MKLVITIFLVITISLSYATFLINKVPLPVDKLAPLPLDNLTPM--DPL-KLLKTL 56  
 OY 50 DAPPEAVAAKLGVKRCTDMSLOKRSLIAEVLVKILKKS 89  
 DB 57 GISVEHLVE--GLKRCVDELGP-----ASEAVKRLLEALS 90

RESULT 12  
 CYTF\_MOUSE STANDARD: PRT: 144 AA.  
 ID CYTF\_MOUSE  
 AC O89098:  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cystatin F precursor (leukocystatin) (Cystatin 7) (Cystatin-like metastasis-associated protein) (CMAP).  
 GN CMT7.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98298157; PubMed=9632704;

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RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,
RA Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebeque S.,
RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.,
RT "Leucocystatin, a new class II cystatin expressed selectively by
RT hematopoietic cells.",
RL J. Biol. Chem. 273:16400-16408(1998).
CC -1- FUNCTION: INHIBITS PAPAIN AND CATHEPSIN L BUT WITH AFFINITIES
CC LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION
CC THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.
-----
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DR EMBL: AF031826; AAC40140.1; -.
DR EMBL: AF031825; AAC40139.1; -.
DR HSSP: P01034; I696.
DR MGD: MGI:1298217; Cst7.
DR InterPro: IPR000010; Cystatin.
DR Pfam: PF00031; cystatin; 1.
DR SMART: SM00043; Cy: 1.
DR PROSITE: PS00267; CYSTATIN; FALSE_NEG.
KW Thiol protease inhibitor; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 144
FT ACT_SITE 36 36 CYSTATIN F.
FT SITE 80 84 REACTIVE SITE.
FT DISULFID 98 109 SECONDARY AREA OF CONTACT.
FT DISULFID 123 143 BY SIMILARITY.
SQ SEQUENCE 144 AA; 16380 MW; B583734C1B4A89C CRC64;

Query Match 15.3%; Score 69; DB 1; Length 144;
Best Local Similarity 27.0%; Pred. No. 0.57;
Matches 24; Conservative 22; Mismatches 25; Indels 18; Gaps 5;

QY 8 LVLTLALCYQANA-----EFCPA-LVSELDFFIFSEPLFKLSLAKFPDPAVNAKL 60
DB 3 LAILLALCCLTSDHNGARPPDFCSKDLISSV-----KPGFPRTI-ETNNPGLKAAKH 54
QY 61 GYVR---CTDOMSLQKRSILAENVLYKILK 86
DB 55 SVEKFNCTNDIFLEKSHSVSKALVQYVK 83

RESULT 13
ID IRA2_YEAST STANDARD; PRT; 3079 AA.
AC P19158; Q08239;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE Inhibitory regulator protein IRA2.
GN IRA2 OR GLC4 OR CCS1 OR YOL081W OR O0985.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90318397; PubMed-2164637;
RA Tanaka K., Nakafuku M., Tamanoi F., Kaziro Y., Matsumoto K., Toh-E A.;
RT "IRA2, a second gene of Saccharomyces cerevisiae that encodes a
RT protein with a domain homologous to mammalian ras GTPase-activating
RT protein.",
RL Mol. Cell. Biol. 10:4303-4313(1990).
RN [2]
RP SEQUENCE OF 1-2423 FROM N.A.

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RC STRAIN-S288c / FY1679;
RX MEDLINE-95208358; PubMed-7900427;
RA Zumstein E., Griffin H., Schweizer M.;
RT "Sequence of a 10.27 kb segment on the left arm of chromosome XV from
RT Saccharomyces cerevisiae includes part of the IRA2 gene and a
RT putative new gene.",
RL Yeast 10:1383-1387(1994).
RN [3]
RP SEQUENCE OF 1982-3079 FROM N.A.
RX MEDLINE-97321807; PubMed-9178509;
RA Tzermia M., Katsoulou C., Alexandraki D.;
RT "Sequence analysis of a 33.2 kb segment from the left arm of yeast
RT chromosome XV reveals eight known genes and ten new open reading
RT frames including homologues of ABC transporters, inositol
RT phosphatases and human expressed sequence tags.",
RL Yeast 13:583-589(1997).
RN [4]
RP IDENTIFICATION OF CCS1 AS IRA2.
RX MEDLINE-92405229; PubMed-1326414;
RA Bussereau F., Dupont C.H., Boy-Marcotte E., Mallet L., Jacquet M.;
RT "The CCS1 gene from Saccharomyces cerevisiae which is involved in
RT mitochondrial functions is identified as IRA2 an attenuator of RAS1
RT and RAS2 gene products.",
RL Curr. Genet. 21:325-329(1992).
CC -1- FUNCTION: INHIBITORY REGULATOR OF THE RAS-CYCCLIC AMP PATHWAY.
CC STIMULATES THE GTPASE ACTIVITY OF RAS PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 RAS-GAP DOMAIN.
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DR EMBL: M33779; AAA34710.1; -.
DR EMBL: X83121; CAA58201.1; -.
DR EMBL: X75449; CAA53202.1; -.
DR EMBL: Z74823; CAA99093.1; -.
DR PIR: S11190; R8BY12.
DR SGD: S0005441; IRA2.
DR InterPro: IPR001936; RasGAP.
DR Pfam: PF00616; RasGAP; 1.
DR SMART: SM00323; RasGAP; 1.
DR PROSITE: PS00509; RAS_GTPASE_ACTIV_1; 1.
DR PROSITE: PS50018; RAS_GTPASE_ACTIV_2; 1.
KW GTPase activation.
FT DOMAIN 1701 1890 RAS-GAP.
FT DOMAIN 399 409 POLY-SER.
FT DOMAIN 412 416 POLY-SER.
FT DOMAIN 520 528 POLY-ALA.
FT DOMAIN 2469 2472 POLY-LEU.
FT CONFLICT 2317 2317 I -> K (III REF. 3).
SQ SEQUENCE 3079 AA; 351631 MW; 651EB.A2EBB479C0 CRC64;

Query Match 14.88%; Score 66.5; DB 1; Length 3079;
Best Local Similarity 32.3%; Pred. No. 24;
Matches 20; Conservative 9; Mismatches 18; Indels 15; Gaps 2;

QY 23 FCPALVS-----ELDFFIFSEPLFKLSLAK-----FDAPPEAVNAKLGVKRCRD 67
DB 1654 FCPALVPSDENITIDISLSEKRFIFSLAKYIQNIANGSEWFKMPALCSQDKFLKCSQD 1913
QY 68 QM 69
DB 1914 RI 1915

RESULT 14
ID SY04_CHICK STANDARD; PRT; 90 AA.
AC Q90826; Q910C9;

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DT 01-NOV-1997 (Rel. 35, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Small inducible cytokine A4 homolog precursor (Macrophage inflammatory  
 DE protein 1-beta homolog).  
 GN SCYA4.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=bone marrow;  
 RX MEDLINE=95369710; PubMed=7642115;  
 RA Petrenko O., Ischenko I., Enrietto P.J.;  
 RT "Isolation of a cDNA encoding a novel chicken chemokine homologous to  
 RT mammalian macrophage inflammatory protein-1 beta.";  
 RL Gene 160:305-306(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC Hughes S.M., Bumstead N.;  
 RT "Mapping of the gene encoding the chicken homologue of the mammalian  
 RT chemokine SCYA4.";  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 14-90 FROM N.A.  
 RA Petrenko O., Enrietto P.J.;  
 RT Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: MONOKINE WITH INFLAMMATORY AND CHEMOKINETIC PROPERTIES  
 CC (BY SIMILARITY)  
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE  
 CC C-C) (CHEMOKINE CC).  
 CC -----  
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 CC -----  
 DR EMBL: L34553; AAA48747.1; -;  
 DR EMBL: AJ243034; CAB45103.1; -;  
 DR HSSP: P13236; IH0M.  
 DR InterPro: IPR000827; CC\_chemkine\_sml.  
 DR InterPro: IPR001811; Chemokine\_IL8.  
 DR Pfam: PF00048; IL8; 1.  
 DR SMART: SM00199; SCY; 1.  
 DR PROSITE: PS00472; SMALL\_CYTOKINES\_CC; 1.  
 KW Cytokine; Chemotaxis; Signal.  
 FT SIGNAL 1 21 BY SIMILARITY.  
 FT CHAIN 22 90 SMALL INDUCIBLE CYTOKINE A4 HOMOLOG.  
 FT DISULFID 32 56 BY SIMILARITY.  
 FT DISULFID 33 72 BY SIMILARITY.  
 FT CONFLICT 87 87 M -> L (IN REF. 1).  
 FT CONFLICT 87 87  
 SQ SEQUENCE 90 AA; 9987 MW; 50AF9679A267408F CRC64;  
 Query Match 13.9%; Score 62.5; DB 1; Length 90;  
 Best Local Similarity 33.3%; Pred. No. 2;  
 Matches 16; Conservative 6; Mismatches 17; Indels 9; Gaps 1;  
 QY 1 MKLSVCLLVLTALCCYQANA-----EPCPALVSELDPEFFISE 39  
 DB 1 MKVSAALAVLVLTATCYTSAPVGSDFPTSCFTTISQLPFSFVAD 48  
 RESULT 15  
 FE12\_FELCA  
 ID FE12\_FELCA STANDARD: PRT: 109 AA.  
 AC P30440;

DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B)  
 DE (Fel d I-B) (Allergen cat-1) (Ag4) (f01).  
 GN CH2.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-100.  
 RX MEDLINE=92052157; PubMed=1946388;  
 RA Morgenstern J.P., Griffith I.J., Brauer A.W., Rogers B.L.,  
 RA Bond J.F., Chapman M.D., Kuo M.-C.;  
 RT "Amino acid sequence of fel d1, the major allergen of the domestic  
 RT cat: protein sequence analysis and cDNA cloning";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9690-9694(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS.  
 RC TISSUE=Liver;  
 RX MEDLINE=92241678; PubMed=1572548;  
 RA Griffith I.J., Craig S., Pollock J., Yu X.-B., Morgenstern J.P.,  
 RA Rogers B.L.;  
 RT "Expression and genomic structure of the genes encoding Fd1, the  
 RT major allergen from the domestic cat.";  
 RL Gene 113:263-268(1992).  
 RN [3]  
 RP SEQUENCE OF 18-37, AND CHARACTERIZATION.  
 RX MEDLINE=91287714; PubMed=1712068;  
 RA Duffort O.A., Carreira J., Nitti G., Polo F., Lombardero M.;  
 RT "Studies on the biochemical structure of the major cat allergen Felis  
 RT domesticus I.";  
 RL Mol. Immunol. 28:301-309(1991).  
 RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=84265679; PubMed=6747135;  
 RA Lelerman K., Oman J.L. Jr.;  
 RT "Cat allergen 1: Biochemical, antigenic, and allergenic properties.";  
 RL J. Allergy Clin. Immunol. 74:147-153(1984).  
 CC -1- SUBUNIT: HETEROTETRAMER COMPOSED OF TWO NON-COVALENTLY LINKED  
 CC DISULFIDE-LINKED HETERODIMER OF CHAINS 1 AND 2.  
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; a long form/CH2L (shown here), a  
 CC short form/CH2S and a truncated form/CH2ST; may be produced by  
 CC alternative splicing.  
 CC -1- TISSUE SPECIFICITY: THE LONG FORM IS PREFERENTIALLY EXPRESSED IN  
 CC THE SALIVARY GLAND, WHILE THE SHORT FORM IS PREFERENTIALLY  
 CC EXPRESSED IN THE SKIN.  
 CC -1- DISEASE: MAJOR ALLERGEN PRODUCED BY THE DOMESTIC CAT.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC -----  
 DR EMBL: M77341; AAC41616.1; -;  
 DR EMBL: X62478; CAA44345.1; -;  
 DR PIR: JC1127; JC1127.  
 DR PIR: JC1145; JC1145.  
 KW Allergen; Glycoprotein; Signal; Polymorphism; Alternative splicing.  
 FT SIGNAL 1 17  
 FT CHAIN 18 109 MAJOR ALLERGEN I POLYPEPTIDE CHAIN 2.  
 FT CARBOHYD 50 50 N-LINKED (GLCNAc...).  
 FT VARSPLIC 82 109 TTISSKCKMGKAVONTVEDLNTLGR -> PSTNIMAVK  
 FT VARSPLIC 82 89 QFRP (IN ISOFORM CH2ST).  
 FT VARSPLIC 72 72 TTISSSKD -> IAINRY (IN ISOFORM CH2S).  
 FT VARIANT 72 72 I -> L (IN CH2LV).  
 FT VARIANT 74 75 I -> V (IN CH2SV).  
 FT VARIANT 74 75 RV -> KF (IN CH2SV).  
 FT VARIANT 91 91 M -> T (IN CH2LV).  
 FT VARIANT 91 91

FT VARIANT 96 96 Q -> E (IN CH2SV).  
 FT VARIANT 105 105 N -> K (IN CH2SV).  
 FT CONFLICT 24 24 C -> F (IN REF. 3).  
 FT CONFLICT 32 32 F -> T (IN REF. 3).  
 SQ SEQUENCE 109 AA; 11854 MM; 857/FB9CD76036CB9 CRC64;

Query Match 13.8%; Score 62; DB 1; Length 109;  
 Best Local Similarity 36.8%; Pred. No. 2.8;  
 Matches 32; Conservative 6; Mismatches 37; Indels 12; Gaps 5;

QY 3 LSYCLLVTLALCCYQANAECPALVSELDFFFI---SEPLFKLSIAKFDA-PPEAVA 57  
 Db 5 LVLVALLVTOALGVKM--AETCPI---FYDVFPFAVANGNELLDLSLTFKNATEPERTA 58

QY 58 AKLGVKRCIDQMSLQKRSLIAEVLVKI 84  
 Db 59 MK-KIQCYYENGLISRVLGDLVMTTI 84

Search completed: January 2, 2003, 14:54:41  
 Job time : 14 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 2, 2003, 14:53:42 ; Search time 17 Seconds

(without alignments)  
508.947 Million cell updates/sec

Title: US-09-806-301-2

Perfect score: 450

Sequence: 1 MKLSVCLLVTLALCCYQAN.....LQKRSLIAEVLVKKCSV 90

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:\*  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	206	45.8	111	1 BOR1	prostatic steroid-
2	177	39.3	95	2 S68231	FHG22 protein prec
3	166.5	37.0	98	1 BOR2	prostatic steroid-
4	110	24.4	91	2 JS0036	ciara cell 10K pro
5	102	22.7	91	1 UGRB	uteroglobin precu
6	101	22.2	96	1 UGMS	uteroglobin precu
7	100	22.2	96	2 A36581	polychlorinated bi
8	97	21.6	91	1 UGRB	uteroglobin precu
9	83.5	18.6	113	2 JC2026	cell specific 10K
10	77.5	17.2	94	2 S17449	probable ligand-bi
11	70	15.3	107	2 JC1127	ABC transporter at
12	69	15.3	1633	2 T01369	major allergen cha
13	66.5	14.8	578	2 T24735	hypothetical prote
14	66.5	14.8	3079	1 RGR12	hypothetical prote
15	66	14.7	102	2 G97516	hypothetical prote
16	64	14.2	25	2 S26651	uteroglobin precu
17	64	14.2	797	2 D86459	probable disease r
18	63	14.0	92	2 JC1136	major allergen cha
19	62.5	13.9	371	2 E88986	protein C50H11.13
20	62.5	13.9	929	2 C90531	cation-transportin
21	62	13.8	109	2 C56413	major allergen Fel
22	62	13.8	284	2 T36313	probable oxidoredu
23	61.5	13.7	200	2 E72066	riboflavin synthas
24	61.5	13.7	200	2 H86556	riboflavin synthas
25	61.5	13.7	416	2 AF2070	hypothetical prote
26	61.5	13.7	1094	2 T00814	RNA-directed DNA p
27	61	13.6	340	2 T46942	Smoc-like regulato
28	61	13.6	812	2 H86265	protein F3P19.18
29	60.5	13.4	92	2 A56413	major allergen Fel

30	60.5	13.4	234	2 T31886	hypothetical prote
31	60.5	13.4	315	2 T39444	hypothetical prote
32	60.5	13.4	392	2 A88125	protein T12C9.4 [1
33	60.5	13.4	1390	1 TVH0ME	hepatocyte growth
34	60	13.3	100	2 T11037	hypothetical prote
35	60	13.3	123	2 I51604	cholecystokinin pr
36	60	13.3	246	2 T28166	hypothetical prote
37	60	13.3	346	2 T38750	hypothetical prote
38	60	13.3	664	2 C84869	probable receptor
39	59.5	13.2	244	2 AB1120	conserved hypothet
40	59.5	13.2	247	2 AE1480	conserved hypothet
41	59	13.1	261	2 T43579	type III secretion
42	58.5	13.0	961	2 AE2270	exonuclease ABC C
43	58.5	13.0	1097	2 S68685	adenylate cyclase
44	58	12.9	140	2 H64411	hypothetical prote
45	58	12.9	199	2 C75213	hypothetical prote

#### ALIGNMENTS

##### RESULT 1

BOR1

prostatic steroid-binding protein chain C1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Oct-1982 #sequence-revision 15-Oct-1982 #text-change 22-Jun-1999

C:Accession: A93286; A92348; A90348; S42615; A03252

R:Parker, M.; Needham, M.; White, R.

Nature 298, 92-94, 1982

A:Title: Prostatic steroid binding protein: gene duplication and steroid binding.

A:Reference number: A93286; MUID:82220075; PMID:6896362

A:Accession: A93286

A:Molecule type: mRNA

A:Residues: 1-111 <PAR>

R:Liao, S.; Chen, C.; Huang, I.Y.

J. Biol. Chem. 257, 122-125, 1982

A:Title: Prostatic alpha-protein. Complete amino acid sequence of the component that

A:Reference number: A92348; MUID:82075873; PMID:7198120

A:Accession: A92348

A:Molecule type: protein

A:Residues: 24-73,'D','75-89,'E','91,'G','93-111 <LIA>

R:DeLaey, B.; Rombauts, W.; Volckaert, G.; Peeters, B.; Mous, J.; Heyns, W.

Biochem. Soc. Trans. 10, 51, 1982

A:Title: Identification of a complementary-DNA clone containing part of the sequence

A:Reference number: A90348

A:Accession: A90348

A:Molecule type: mRNA

A:Residues: 13-14,'S','16,'GG','19-65 <DEL>

R:DeLaey, B.; Dirckx, L.; Peeters, B.; Volckaert, G.; Mous, J.; Heyns, W.; Rombauts,

Eur. J. Biochem. 133, 645-649, 1983

A:Title: The nucleotide sequence of cDNA complementary to the C(1) component of rat f

A:Reference number: S42615; MUID:83234456; PMID:6688048

A:Accession: S42615

A:Molecule type: mRNA

A:Residues: 1-3,'IK','6-89,'E','91,'G','93-111 <DEZ>

C:Cross-references: EMBL:V01545; NID:957108; PIDN:CAA24787.1; PID:957109

C:Comment: Steroid-binding protein, the principal secretory protein in rat prostatic

. The chains of each dimer are linked by disulfide bonds.

C:Keywords: heterotrimer; prostate; steroid binding

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-111/Product: prostatic steroid-binding protein chain C1 #status experimental <MF>

Query Match

Best Local Similarity 49.5%; Pred. No. 1,4e-16;

Matches 45; Conservative 14; Mismatches 30; Indels 2; Gaps 2;

Query 1 MKLSVCLLVTLALCCYQANA-EFCPALVSELDFFISPELFKSLAKDPAPPAVAAR 59

Db 4 VELSCLLIM-LAVCCTEANSQICELVAHETTSFLKSEBELKELMTNAPAAVEAK 62

Query 60 LGVRCITDMSLQKRSLIAEVLVKKCSV 10

1 ||||| ||||| | :||| || | || |

DB 63 LEVKRCVDDMSNDRLVAETLVYIFLKCDV 93

# RESULT 2

S68231

FIG22 protein precursor - golden hamster

C:Species: Mesocricetus auratus (golden hamster)

C>Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 21-Aug-1998

C:Accession: S68231

R:Dominguez, P.

FEBS Lett. 376, 257-261, 1995

A:Title: Cloning of a Syrian hamster cDNA related to sexual dimorphism: establishment of

A:Reference number: S68231; MUID:96105393; PMID:7498554

A:Accession: S68231

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-95 <DOM>

A:Cross-references: EMBL:Z66540

C:Superfamily: uteroglobin

F:1-2/Domain: signal sequence #status predicted <SIG>

F:22-95/Product: FIG22 protein #status predicted <MAT>

Query Match 39.3%; Score 177; DB 2; Length 95;

Best Local Similarity 43.3%; Pred. No. 2, 7e-13;

Matches 39; Conservative 19; Mismatches 30; Indels 2; Gaps 2;

QY 1 MKLSVCLLVLTALCCYQAN-AECPALVSELDFFFISEPLFKLSLAFDAPPEAVAK 59

DB 1 MKLSVCLLVLTALVAVHCYEAANAVCPALVSVSKSFDFKVEKFAVLQTFNAPPEAVAK 60

QY 60 LCVKRCCTDQ-MSLQKRSLLAEVLYKLKCC 88

DB 61 VEYKRCIDSTLVNLEKMEKSLAEVLYGVC 90

# RESULT 3

BORT2

prostatic steroid-binding protein chain C2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 15-Oct-1982 #sequence\_revision 15-Oct-1982 #text\_change 24-Sep-1999

C:Accession: A03251; A26671

R:Parke, M.; Needham, M.; White, R.

Nature 298, 92-94, 1982

A:Title: Prostatic steroid binding protein: gene duplication and steroid binding.

A:Reference number: A93286; MUID:82220075; PMID:6896362

A:Accession: A03251

A:Molecule type: mRNA

A:Residues: 1-98 <PAR>

A:Cross-references: GB:J00776; NID:9206448; PIDN:AA51641.1; PID:9206450

R:Deleay, B.; Dirckx, L.; Decourt, J.L.; Claessens, F.; Peeters, B.; Rombaux, W.

Nucleic Acids Res. 15, 1627-1641, 1987

A:Title: Rat prostatic binding protein: the complete sequence of the C2 gene and its fl

A:Reference number: A26671; MUID:87146484; PMID:2881277

A:Accession: A26671

A:Molecule type: DNA

A:Residues: 1-25, 'Q', 26-86, 'I', 88-94, 'VMQINPGRGFESEIN' <DEL>

A:Cross-references: GB:X05034; NID:956857; PIDN:CAA28708.1; PID:956858

C:Comment: Steroid-binding protein, the principal secretory protein in rat prostatic flu

C:Superfamily: uteroglobin

C:Keywords: heterotetramer; prostate; steroid binding

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-98/Product: prostatic steroid-binding protein chain C2 #status predicted <MAT>

Query Match 37.0%; Score 166.5; DB 1; Length 98;

Best Local Similarity 42.6%; Pred. No. 4, 6e-12;

Matches 40; Conservative 12; Mismatches 37; Indels 5; Gaps 2;

QY 1 MKLSVCLLVLTALCCYQAN-AECPALVSELDFFFISEPLFKLSLAFDAPPEAV 56

DB 1 MKLSVCLLVLTALVAVHCYEAANAVCPALVSVSKSFDFKVEKFAVLQTFNAPPEAV 59

QY 57 AAKLGKRCCTDQMSLQKRSLLAEVLYKLKCCSV 90

DB 60 EANKVKRCINIKMYGDRLSMTSLVFTMLKCDV 93

# RESULT 4

JS0036

Clara cell 10K protein precursor - human

N:Alternate names: urinary protein 1

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 20-Aug-1999

C:Accession: JS0036; PS0309; A56890; 138397

R:Singh, G.; Kayala, S.L.; Brown, W.E.; Phillips, S.; Kennedy, A.L.; Anthony, J.; Sque

Bloom, B. Phys. Acta 950, 329-337, 1988

A:Title: Amino-acid and cDNA nucleotide sequences of human Clara cell 10KDa protein.

A:Reference number: JS0036; MUID:89000784; PMID:3167058

A:Accession: JS0036

A:Molecule type: mRNA

A:Residues: 1-91 <SIN>

A:Cross-references: GB:X13197; NID:923131; PIDN:CAA31584.1; PID:923132

A:Accession: PS0309

A:Molecule type: protein

A:Residues: 22-23, 'X', 25-28, 'X', 30-31, 'X', 33-36 <SIZ>

R:Bernard, A.; Roels, H.; Lauwerys, R.; Wilters, R.; Gielens, C.; Soumilleu, A.; Van

Clin. Chim. Acta 207, 239-249, 1992

A:Title: Human urinary protein 1: evidence for identity with the Clara cell protein a

A:Reference number: A56890; MUID:93009001; PMID:1395029

A:Accession: A56890

A:Molecule type: protein

A:Residues: 22-45 <BER>

A:Experimental source: urine

A>Note: sequence extracted from NCBI backbone (NCBIP:119391)

R:Hay, J.G.; Daniel, C.; Chu, C.; Crystal, R.G.

Am. J. Physiol. 268, 565-575, 1995

A:Title: Human CC10 gene expression in airway epithelium and subchromosomal locus sug

A:Reference number: 138397

A:Accession: 138397

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-91 <RES>

A:Cross-references: EMBL:U01101; NID:9457932; PIDN:AA81885.1; PID:9457933

C:Comment: This protein consists of two identical polypeptides linked by two disulfid

C:Genetics:

A:Gene: CC10

C:Superfamily: uteroglobin

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-91/Product: Clara cell 10K protein #status experimental <MAT>

Query Match 24.4%; Score 110; DB 2; Length 91;

Best Local Similarity 31.0%; Pred. No. 1, 5e-05;

Matches 26; Conservative 17; Mismatches 41; Indels 0; Gaps 0;

QY 1 MKLSVCLLVLTALCCYQANAECPALVSELDFFFISEPLFKLSLAFDAPPEAVAKL 60

DB 1 MKLVAVTLVLTALCCSSASAEICPSFORVITLMDTSSYEAMLEFSPQDREAGA 60

QY 61 GVKRCCTDQMSLQKRSLLAEVLYKI 84

DB 61 QKRLVDTLPLQKPRESIIRIMEKI 84

# RESULT 5

UGRB

uteroglobin precursor [validated] - rabbit

N:Alternate names: blastokinin

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 28-Feb-1980 #sequence\_revision 15-Oct-1992 #text\_change 15-Sep-2000

C:Accession: A92391; A93461; A90935; A90417; A93824; A94608; I46904;

R:Bailey, A.; Atger, M.; Atger, P.; Cerdon, M.A.; Allizon, M.; Vu Hal, M.T.; Logeart, F

J. Biol. Chem. 258, 10384-10389, 1983

A:Title: The rabbit uteroglobin gene, structure and interaction with the progesterone

A:Reference number: A92391; MUID:83290960; PMID:6309802

A:Accession: A92391

A:Molecule type: DNA

A:Residues: 1-91 <BAI>  
 A:Cross-references: GB:K00049; NID:g165789  
 R:Suske, G.; Wenz, M.; Cato, A.C.B.; Beato, M.  
 Nucleic Acids Res. 11, 2257-2271, 1983  
 A:Title: The uteroglobin gene region: hormonal regulation, repetitive elements and comp  
 A:Reference number: A93461; MUID:83220783; PMID:6304644  
 A:Accession: A93461  
 A:Molecule type: DNA  
 A:Residues: 1-91 <SUS>  
 A:Cross-references: GB:J00687; NID:g1772; PIDN:CAA25669.1; PID:g313668  
 R:Chandra, T.; Bullock, D.W.; Woo, S.L.C.  
 DNA 1, 19-26, 1981  
 A:Title: Horizontally regulated mammalian gene expression: steady-state level and nucleoti  
 A:Reference number: A90935; MUID:83157105; PMID:6299663  
 A:Accession: A90935  
 A:Molecule type: mRNA  
 A:Residues: 1-91 <CHA>  
 A:Cross-references: GB:K01657; NID:g165794; PIDN:AAA31497.1; PID:g165795  
 R:Lopez de Haro, M.S.; Nieto, A.  
 FEBS Lett. 193, 247-249, 1985  
 A:Title: Primary structure of rabbit lung uteroglobin as deduced from the nucleotide seq  
 A:Reference number: A24217; MUID:86056319; PMID:2415398  
 A:Accession: A24217  
 A:Molecule type: mRNA  
 A:Residues: 22-91 <LOP>  
 A:Cross-references: GB:M27564; NID:g165792; PIDN:AAA31496.1; PID:g165793  
 A:Experimental source: Lung  
 R:Atger, M.; Mercier, J.C.; Haze, G.; Fridlansky, F.; Milgrom, E.  
 Biochem. J. 177, 985-988, 1979  
 A:Title: N-terminal sequences of uteroglobin and its precursor.  
 A:Reference number: A90303; MUID:79187160; PMID:571719  
 A:Accession: A90303  
 A:Molecule type: protein  
 A:Residues: 1-5, 'F', 7-10, 'X', 15, 'G', 17-54, 'X', 56, 'B', 58-66, 'B', 68-70, 'XX', 73 <ATG>  
 R:Ponstingl, H.; Nieto, A.; Beato, M.  
 Biochemistry 17, 3908-3912, 1978  
 A:Title: Amino acid sequence of progesterone-induced rabbit uteroglobin.  
 A:Reference number: A90417; MUID:79042086; PMID:568483  
 A:Accession: A90417  
 A:Molecule type: protein  
 A:Residues: 22-81, 'Q', 83-91 <PON>  
 R:Popp, R.A.; Foreman, K.R.; Wise, L.D.; Daniel Jr., J.C.  
 Proc. Natl. Acad. Sci. U.S.A. 75, 5516-5519, 1978  
 A:Title: Amino acid sequence of a progesterone-binding protein.  
 A:Reference number: A93824; MUID:79074850; PMID:281700  
 A:Accession: A93824  
 A:Molecule type: protein  
 A:Residues: 22-45, 'D', 51, 'EN', 54-59, 61-66, 'NEPSL', 72-91 <POP>  
 R:Popp, R.A.; Foreman, K.R.; Wise, L.D.; Daniel Jr., J.C.  
 Submitted to the Atlas, October 1982  
 A:Reference number: A94608  
 A:Accession: A94608  
 A:Molecule type: protein  
 A:Residues: 50-62, 67-71 <PO2>  
 R:Morize, I.; Surcouf, E.; Vanev, M.C.; Buehner, M.; Morion, J.P.  
 Submitted to the Brookhaven Protein Data Bank, April 1989  
 A:Reference number: A50025; PDB:1JMG  
 A:Contents: annotation; X-ray crystallography, 1.34 angstroms, residues 22-91  
 R:Morize, I.; Surcouf, E.; Vanev, M.C.; Epelboin, Y.; Buehner, M.; Fridlansky, F.; Milgr  
 J. Mol. Biol. 194, 725-739, 1987  
 A:Title: Refinement of the C22-1 crystal form of oxidized uteroglobin at 1.34 angstroms  
 A:Reference number: A44652; MUID:88011213; PMID:3656405  
 A:Contents: annotation; X-ray crystallography, 1.34 angstroms  
 R:Bally, R.; Delletre, J.  
 Submitted to the Brookhaven Protein Data Bank, May 1989  
 A:Reference number: A50553; PDB:2UTG  
 A:Contents: annotation; X-ray crystallography, 1.64 angstroms, residues 22-91  
 J. Mol. Biol. 206, 153-170, 1989  
 A:Title: Structure and refinement of the oxidized P2-1 form of uteroglobin at 1.64 angst  
 A:Reference number: A44653; MUID:99199637; PMID:2704039  
 A:Contents: annotation; X-ray crystallography, 1.64 angstroms; disulfide bonds  
 R:Menne, C.; Suske, G.; Arnemann, J.; Wenz, M.; Cato, A.C.B.; Beato, M.

Proc. Natl. Acad. Sci. U.S.A. 79, 4853-4857, 1982  
 A:Title: Isolation and structure of the gene for the progesterone-inducible protein  
 A:Reference number: I46904; MUID:83014990; PMID:6956887  
 A:Accession: I46904  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-91 <MEN>  
 A:Cross-references: GB:J00689; NID:g165786; PIDN:AAA31495.1; PID:g165788  
 R:Chandra, T.; Woo, S.L.C.; Bullock, D.W.  
 Biochem. Biophys. Res. Commun. 95, 197-204, 1980  
 A:Title: Cloning of the rabbit uteroglobin structural gene.  
 A:Reference number: I46905; MUID:81021016; PMID:7417250  
 A:Accession: I46905  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 39-77 <CH2>  
 A:Cross-references: GB:M25057; NID:g165802; PIDN:AAA31498.1; PID:g165803  
 R:Suske, G.; Menne, C.; Cato, A.; Wenz, M.; Beato, M.  
 Prog. Clin. Biol. Res. 85, 139-146, 1982  
 A:Title: Structure and regulated expression of the uteroglobin gene.  
 A:Reference number: I46907; MUID:82275176; PMID:6287481  
 A:Accession: I46907  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-45, 'V', 47-91 <SUD>  
 A:Cross-references: GB:M32012; NID:g165807; PIDN:AAA31500.1; PID:g165809  
 R:Atger, M.; Perricaudet, M.; Tjollals, P.; Milgrom, E.  
 Biochem. Biophys. Res. Commun. 93, 1082-1088, 1980  
 A:Title: Bacterial cloning of the rabbit uteroglobin structural gene.  
 A:Reference number: I46906; MUID:80241888; PMID:6156676  
 A:Accession: I46906  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 33-66, 'N', 69-72 <AT2>  
 A:Cross-references: GB:M25038; NID:g165804; PIDN:AAA31499.1; PID:g165805  
 C:Comment: Uteroglobin is secreted by the uterus upon induction by progesterone. It  
 C:Genetics:  
 A:Insertions: 19/1; 81/3  
 C:Complex: homodimer linked by two disulfide bonds  
 C:Superfamily: uteroglobin  
 C:Keywords: homodimer; steroid binding; uterus  
 F:1-21/Domain: signal sequence #status experimental <SIG>  
 F:22-91/Product: uteroglobin #status experimental <MAT>  
 F:24/Disulfide bonds: interchain (to 90) #status experimental  
 F:90/Disulfide bonds: interchain (to 24) #status experimental  
 Query Match 22.7%; Score 102; DB 1; Length 91;  
 Best local similarity 30.2%; Pred. No. 0.00013;  
 Matches 26; Conservative 17; Mismatches 43; Indels 0; Gaps 0;  
 Oy 1 MKLSVCLLVTLALCCYQANNEFPALVSELDFFFISEPLFKSLAKFDAPPAVAKL 60  
 DB 1 MKLAITLALVTLALCCPASAGICPPAHVTEILLCTPSSYSYSLKEFPDDPTMKDGM 60  
 Oy 61 GVKRCTQOMSLOKRSLLAEVLVKTIK 86  
 DB 61 QMKRVDSLPTPTRENTMKLTKETIK 86  
 RESULT 6  
 UGMS  
 uteroglobin precursor - mouse  
 N:Alternate names: CClO; Clara cell 10K proteln precursor; Clara cell secretory prot  
 C:Species: Mus musculus (house mouse)  
 C:Date: 03-May-1994 #sequence, revision 21-Jan-1997 #text, change 22-Jun-1999  
 C:Accession: A53025; A56656; I51925; S24783  
 R:Stripp, B.R.; Huffman, J.A.; Bohinski, R.J.  
 Genomics 20, 27-35, 1994  
 A:Title: Structure and regulation of the murine Clara cell secretory protein gene.  
 A:Reference number: A53025; MUID:94292183; PMID:8020953  
 A:Accession: A53025  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-96 <STR>  
A:Cross-references: GB:L24372; NID:g461147; PIDN:AAA65446.1; PID:g785054  
R:Singh, G.; Katyal, S.L.; Brown, W.E.; Kennedy, A.L.  
Exp. Lung Res. 19, 67-75, 1993  
A:Title: Mouse Clara cell 10-kDa (CC10) protein: cDNA nucleotide sequence and molecular  
A:Reference number: A56556; MUID:93178380; PMID:8440203  
A:Accession: A56556  
A:Molecule type: mRNA  
A:Residues: 1-96 <SIN>  
A:Cross-references: EMBL:X67702; NID:g49690; PIDN:CAA47936.1; PID:g49691  
A:Experimental source: lung  
A:Note: sequence extracted from NCBI backbone (NCBI:P126148)  
R:Margraf, L.R.; Finegold, M.J.; Stanley, L.A.; Major, A.; Watkins, H.K.; Demayo, F.J.  
Am. J. Respir. Cell Mol. Biol. 9, 231-238, 1993  
A:Title: Cloning and tissue-specific expression of the cDNA for the mouse Clara cell 10k  
A:Reference number: 151925; MUID:9400840; PMID:8398159  
A:Accession: 151925  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-96 <RES>  
A:Cross-references: GB:I04503; NID:g202313; PIDN:AAA03625.1; PID:g433093  
C:Genetics:  
A:Introns: 19/1; 81/3  
C:Complex: homodimer linked by two disulfide bonds  
C:Superfamily: uteroglobin  
C:Keywords: lung; steroid binding; uterus  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-96/Product: uteroglobin #status predicted <MA>  
F:24/Disulfide bonds: Interchain (to 90) #status predicted  
F:90/Disulfide bonds: Interchain (to 24) #status predicted

Query Match 22.4%; Score 101; DB 1; Length 96;  
Best Local Similarity 28.2%; Pred. No. 0.0018;  
Matches 24; Conservative 19; Mismatches 42; Indels 0; Gaps 0;

Oy 1 MKLSVCLLVLTALCCYANAEFCALVSELDFPFISPELFKSLAKFADAPPAAVAKL 60  
Db 1 MKIATITVVMISICSSASSDICGFLQVLEALMESESGYVSLKPFNGSDLONAGT 60  
Oy 61 GVKRCTQMSLOKRSLIAEVLVKIL 85  
Db 61 QLRKRVDTLPQETRNIMKITEKIL 85

RESULT 7  
A3581  
polychlorinated biphenyl-binding protein precursor - rat  
N:Alternate names: Clara cell 10k secretory protein  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 20-Aug-1999  
A:Accession: A3581; S10185; S21676  
R:Nordlund-Moeller, L.; Andersson, O.; Allgren, R.; Schilling, J.; Giller, M.; Gustafsson  
J. Biol. Chem. 265, 12690-12693, 1990  
A:Title: Cloning, structure, and expression of a rat binding protein for polychlorinated  
A:Reference number: A3581; MUID:50324265; PMID:2115524  
A:Accession: A3581  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-96 <NOR>  
A:Cross-references: GB:J05536; NID:g206039; PIDN:AAA41817.1; PID:g206040  
R:Hagen, G.; Wolf, M.; Katyal, S.L.; Singh, G.; Beato, M.; Suske, G.  
Nucleic Acids Res. 18, 2939-2946, 1990  
A:Title: Tissue-specific expression, hormonal regulation and 5'-flanking gene region of  
A:Reference number: S10185; MUID:90272398; PMID:2349092  
A:Accession: S10185  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-18 <HAG>  
A:Cross-references: EMBL:X51318; NID:g55536; PIDN:CAA35701.1; PID:g55537  
R:Unland, T.C.; Swaminathan, S.; Furey, W.; Singh, G.; Pletcher, J.; Sax, M.  
Mol. Biol. 224, 441-448, 1992  
A:Title: Refined structure of rat Clara cell 17 kDa protein at 3.0 A resolution.

```

A:Reference number: S21676; MUID:92219263; PMID:1560460
A:Contents: annotation, X-ray crystallography, 3.0 angstroms
C:Superfamily: uteroglobin
F:24/Dissulfide bonds: Interchain (to 90) #status experimental
F:90/Dissulfide bonds: Interchain (to 24) #status experimental

Query Match      22.2%; Score 100; DB 2; Length 96;
Best Local Similarity 25.9%; Pred. No. 0.00023;
Matches 22; Conservative 22; Mismatches 41; Indels 0; Gaps 0;

OY 1 MKLSVLLVTALCCYOANAEFCPALVSLELDFEFSIEPLFKSLAKFDAPPEVAAKL 60
    ||::: :||:::||::||::||::| |::| |::| |::| |::| |::| |::| |::|
DB 1 MKIATITIVLMSTICSSASSDICPGFLQVEALLLGSESNTEALKFPNPASDLQNAGT 60
    ::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 61 GVKRCTDQMSLOKRSLIAEVLYKIL 85
    ::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 61 QLKRLVDTLPEQTRINIVKLTREKIL 85
    ::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 8
UGRBL
uteroglobin precursor - brown hare
N:Alternate names: blastokinin
C:Species: Lepus capensis (brown hare)
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C:Accession: A23825
R:Lopez de Haro, M.S.; Nieto, A.
Biochem. J. 235, 895-898, 1986
A:title: Nucleotide and derived amino acid sequences of a cDNA coding for pre-uterogl
A:Reference number: A23825; MUID:86323069; PMID:3019311
A:Accession: A23825
A:Molecule type: mRNA
A:Residues: 1-91 <LOP>
A:Cross-references: GB:S25609; NID:g164246; PIDN:AAA30960.1; PID:g164247
A:Experimental source: lung
C:Comment: Uteroglobin, synthesized in the uterus and lung, is secreted by the uterus
C:Complex: homodimer linked by two disulfide bonds
C:Superfamily: uteroglobin
C:Keywords: lung; steroid binding; uterus
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-91/Product: uteroglobin #status predicted <MAT>
F:24/Dissulfide bonds: Interchain (to 90) #status predicted
F:90/Dissulfide bonds: Interchain (to 24) #status predicted

Query Match      21.6%; Score 97; DB 1; Length 91;
Best Local Similarity 30.2%; Pred. No. 0.00048;
Matches 26; Conservative 15; Mismatches 45; Indels 0; Gaps 0;

OY 1 MKLSVLLVTALCCYOANAEFCPALVSLELDFEFSIEPLFKSLAKFDAPPEVAAKL 60
    ||::: ||||||::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 1 MKIATITLVLTALLCSPASAGICPGFAHVIENTLLGTSPSYGSLKEFGDDAMKDAGM 60
    ::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
OY 61 GVKRCTDQMSLOKRSLIAEVLYKIL 86
    ::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 61 QMKRVLDTLPEQTRENIITIKLTEIKV 86
    ::|| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

RESULT 9
JC2026
cell specific 10k protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: JC2026
R:Ray, M.K.; Magdaleno, S.; O'Malley, B.W.; Demayo, F.J.
Biochem. Biophys. Res. Commun. 197, 163-171, 1993
A:title: Cloning and characterization of the mouse clara cell specific 10 kda protein
A:Reference number: JC2026; MUID:94071937; PMID:7916613
A:Accession: JC2026
A:Molecule type: DNA
A:Residues: 1-113 <RAY>
C:Comment: This protein is the major secretory product of the Clara cell and binds to
C:Superfamily: uteroglobin
F:73/Region: ochre stop codon

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[illegible]

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Oy 58 AKGVKRCFQDMSLQKRSIAEVLVKIKMK 88
      |::|::|::|::|::|::|::|::|::|::|
Db 59 MK-KIQDCYENGLISRYLDGLVMIAINEYC 88

RESULT 12
T01369
ABC transporter AtMRP2 [imported] - Arabidopsis thaliana
N:Alternate names: multidrug-resistance protein homolog T29F13.13
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T01369; D84759
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: 214179
A:Accession: T01369
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1623 <R0U>
A:Cross-references: EMBL:AC003096; NID:g3132479; PID:g3132479
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.F.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffitt, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: D84759
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1623 <STO>
A:Cross-references: GB:AE002093; NID:g3132479; PID:AA016268.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g34660; T29F13.13
A:Map position: 2
A:Introns: 110/3; 170/2; 183/3; 236/1; 274/2; 101/2; 309/3; 328/3; 350/3; 375/3; 411/
F:129-1452/Domain: ATP-binding resistance protein cMOAT2; ATP-binding cassette homolo
F:129-1452/Domain: ATP-binding cassette homolog9 <ABC>

Query Match 15.3%; Score 69; Dn 2; Length 1623;
Best Local Similarity 36.5%; Pred. No. 14.
Matches 27; Conservative 9; Mismatches 22; Indels 16; Gaps 5;

Oy 3 LSVCLLYTTLALCCYQNAERCPALVSELLDFF-----ISEPLFL-----SLAFDA 51
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 47 LVLCYRIMLALKKHKVE-RFC--LRSLRYVFTALAAVATAPLFRLLINGISVLDG 103

Oy 52 P--PEAVAKLGVK 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 104 PGLPPEFAFGIGVK 117

RESULT 13
T24735
hypothetical protein T09E11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 06-Oct-2000
C:Accession: T24735
R:McClay, K.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19930
A:Accession: T24735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-578 <WIL>
A:Cross-references: EMBL:Z81147; PID:CA03529.1; GSPDB:GN00019; CESP:T09E11.5
A:Experimental source: clone T09E11
C:Genetics:
A:Gene: CESP:T09E11.5
A:Map position: 1
A:Introns: 42/2; 177/1; 257/2; 317/1; 352/3; 391/1; 430/2; 497/3

```

C:Superfamily: Caenorhabditis elegans hypothetical protein T26h2.7

Query Match 14.8%; Score 66.5; DB 2; Length 578;

Best Local Similarity 27.1%; Pred. No. 10;

Matches 23; Conservative 15; Mismatches 38; Indels 9; Gaps 3;

OY 7 LLLVTLALC---CYANMEFCPALVSELDFFISPEPLKLSIAKFDAPPEAAKLG 62

DB 386 LRVVTVSACEPLAAVPEKPE-CQOELEKFEVDFLEASQPDVAFILTRF----FATGVVANS 440

OY 63 KRCTDQMSLOKRSLLAEVLKILKK 87

DB 441 TSTSDLVLEMRQMSKLLPNIKK 465

#### RESULT 14

RGBY12

probable GTPase-activating protein IRA2 - yeast (Saccharomyces cerevisiae)

M:Alternate names: GLC4 protein; protein O0985; protein YOL081w; protein YOL0951

C:Species: Saccharomyces cerevisiae

C:Date: 30-Sep-1991 #sequence-revision 16-Aug-1996 #text-change 03-Dec-1999

C:Accession: S66775; S66774; A35656; S48254; S50426; S11190; S38505

R:Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

Submitted to the Protein Sequence Database, July 1996

A:Reference number: S66775

A:Accession: S66775

A:Molecule type: DNA

A:Residues: 1-2423 <ZUM>

A:Cross-references: EMBL:Z74823; GSPDB:GN00015; MIPS:YOL081w

A:Experimental source: strain S288C

R:Alexandarakis, D.; Katsoulou, C.; Tzermia, M.

Submitted to the Protein Sequence Database, July 1996

A:Reference number: S66774

A:Accession: S66774

A:Molecule type: DNA

A:Residues: 1983-3079 <ALE>

A:Cross-references: EMBL:Z74823; GSPDB:GN00015; MIPS:YOL081w

A:Experimental source: strain S288C

R:Tanaka, K.; Nakatoku, M.; Tamanoi, F.; Kaziro, Y.; Matsumoto, K.; Toh-e, A.

Mol. Cell. Biol. 10, 4303-4313, 1990

A:Title: IRA2, a second gene of Saccharomyces cerevisiae that encodes a protein with a G

A:Reference number: A35656; MUID:90318397; PMID:2164637

A:Accession: A35656

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-2308, 'V', 2310-2316, 'I', 2318-3079 <TAN>

A:Cross-references: EMBL:M33779; NID:g171761; PIDN:AAA34710.1; PID:g171762

R:Zumstede, E.; Griffin, H.; Schweizer, M.

Yeast 10, 1383-1387, 1994

A:Title: Sequence of a 10.27 kb segment on the left arm of chromosome XV from Saccharomy

A:Reference number: S48253; MUID:95208358; PMID:7900427

A:Accession: S48253

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-2423 <ZUM>

A:Cross-references: EMBL:X75449; NID:g414079; PIDN:CAA53202.1; PID:g414081

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993

R:Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.

Submitted to the EMBL Data Library, December 1994

A:Reference number: S50410

A:Accession: S50410

A:Molecule type: DNA

A:Residues: 1-2423 <ZUM>

A:Cross-references: EMBL:X83121; NID:g600461; PIDN:CAA58201.1; PID:g600480

C:Genetics:

A:Gene: SGD:IRA2; MIPS:YOL081w

A:Cross-references: SGD:S0005441; MIPS:YOL081w

A:Map position: 15L

C:Superfamily: regulatory protein IRA2; ras-specific GAP catalytic domain homology

C:Keywords: transmembrane protein

F:693-709/Domain: transmembrane #status predicted <TM1>

F:1135-1151/Domain: transmembrane #status predicted <TM2>

F:1701-1910/Domain: ras-specific GAP catalytic domain homology <GAP>

F:1842-1858/Domain: transmembrane #status predicted <TM3>

F:2318-2334/Domain: transmembrane #status predicted <TM4>

F:2562-2578/Domain: transmembrane #status predicted <TM5>

Query Match 14.8%; Score 66.5; DB 1; Length 3079;

Best Local Similarity 32.3%; Pred. No. 53;

Matches 20; Conservative 9; Mismatches 18; Indels 15; Gaps 2;

OY 23 FCPALVS---ELDDFFISPEPLKLSIAK-----FDAPPEAAKLGRCND 67

DB 1854 FCPALVSPSENIIDISHSEKRTFSLAKVIONIANSENSESRWALCSQKDFLECSQ 1913

OY 68 QM 69

DB 1914 RI 1915

#### RESULT 15

G97516

hypothetical protein AGR\_C\_2384 [imported] - Agrobacterium tumefaciens (strain C58, C

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence-revision 30-Sep-2001 #text-change 11-Jan-2002

C:Accession: G97516

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: G97516

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <KUR>

A:Cross-references: GB:AE007869; PIDN:AAK67088.1; PID:g15156348; GSPDB:GN00169

C:Genetics:

A:Gene: AGR\_C\_2384

A:Map position: circular chromosome

Query Match 14.7%; Score 66; DB 2; Length 102;

Best Local Similarity 41.2%; Pred. No. 2.1;

Matches 21; Conservative 2; Mismatches 24; Indels 4; Gaps 1;

OY 12 LALCCQAN---AECFPAVSELDFFISPEPLKLSIAKFDAPPEAVAA 58

DB 37 LALSGLQANMLROAVNDPGLTDFLMSHEDLMAFCATDTPETVAA 87

Search completed: January 2, 2003, 14:56:02

Job time : 19 secs